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ME

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From: Slobodyansky, Elizabeth
Sent: Tuesday, August 22, 2006 6:23 PM
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Please search for case 10/665,715:

SEQ ID NO: 16 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner
Art Unit 1652
REM 2D83
571-272-0941
MAILBOX 2C70

10-665-715

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 8-25-06
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run On: August 25, 2006, 07:13:17 ; Search time 194 Seconds
(without alignments)
1277.378 Million cell updates/sec

Title: US-10-665-715-16
Perfect score: 2879
Sequence: 1 MEPDSVIDKTIELMCSVPR.....PPSAQNETRSPRTVTYISR 542

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2879	100.0	542	3 AAY96696	Human E3
2	2879	100.0	542	4 AAM79127	Human pro
3	2879	100.0	542	4 AAM40208	Human pol
4	2879	100.0	542	8 ADS88293	Human pro
5	2879	100.0	542	9 AEA01728	Human bet
6	2879	100.0	550	4 AAM41994	Human pol
7	2873	99.8	542	9 ADX05377	Cyclin-de
8	2755.5	95.7	563	8 ADS88282	Human pro
9	2666.5	92.6	529	9 ADX05979	Cyclin-de
10	2661	92.4	508	9 ADX05981	Cyclin-de
11	2458.5	85.4	579	4 AAM78583	Human pro
12	2445.5	84.9	605	4 AAM78582	Human pro
13	2445.5	84.9	605	8 ADS88274	Human pro
14	2423	84.2	654	4 AAM79568	Human pro
15	2423	84.2	654	4 AAM79567	Human pro
16	2423	84.2	654	4 AAM79566	Human pro
17	2422	84.1	632	4 AAM78584	Human pro
18	2421	84.1	590	4 AAM00847	Human bon
19	2385.5	82.9	608	4 AAM00960	Human bon
20	2384.5	82.8	569	2 AAY24054	A human b
21	2384.5	82.8	569	3 AAY44249	Human cel
22	2384.5	82.8	569	3 AAB12813	Human bet
23	2384.5	82.8	569	3 AAY96697	Human bet

24	2384.5	82.8	569	3 AAY83250	Aay83250 F-box pro
25	2384.5	82.8	569	3 AAY83041	Aay83041 F-box pro
26	2384.5	82.8	569	5 ABG69473	Human bai
27	2384.5	82.8	569	5 AAO22446	Human F-b
28	2384.5	82.8	569	8 ADS88273	Human pro
29	2384.5	82.8	569	9 ADY62359	Human F-b
30	2384.5	82.8	569	9 AEA01725	Human bet
31	2377.5	82.6	569	4 AAB48298	Human 2F1
32	2375.5	82.5	569	3 AAB12812	Mouse ubi
33	2375.5	82.5	569	3 AAY83254	F-box pro
34	2375.5	82.5	1443	9 AEC34365	Mutant be
35	2286.5	79.4	517	2 AAR85852	WD-40 dom
36	2077.5	72.2	510	4 ABB59857	Drosophil
37	1638.5	56.9	701	8 ADN22767	Bacterial
38	1143	39.7	265	4 AAU86942	Human DNA
39	816	28.3	159	4 ADM20097	Protein e
40	723.5	25.1	204	8 ADP29897	Human sec
41	693.5	24.1	219	5 AAU98087	Human bet
42	675.5	23.5	158	4 ADM19852	Protein e
43	664	23.1	131	4 ADM19861	Protein e
44	654	22.7	1326	4 ABB67237	Drosophil
45	654	22.7	1326	4 ABB70051	Drosophil

ALIGNMENTS

RESULT 1

AAI96696
ID AAY96696 standard; protein; 542 AA.

AC AAY96696;

DT 26-SEP-2000 (first entry)

DE Human E3 ubiquitin ligase.

XX E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;
KW nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
KW anti-inflammatory; immunosuppressive; cytostatic.

OS Homo sapiens.

PN WO200034447-A2.

PD 15-JUN-2000.

PF 09-DEC-1999; 99WO-US029371.

PR 10-DEC-1998; 98US-00210060.

XX (SIGN-) SIGNAL PHARM INC.
XX (YISS) YISSUM RES & DEV CO.

PI Manning AM, Mercurio F, Amit S, Ben-Neriah Y, Davis M;
PI Hatzubai A; Lavon I, Yaron A;

XX WPI, 2000-431294/37.
XX N-PSDB; AAA51228.

XX Polypeptide enhancing phosphorylated IkkappaB ubiquitination useful for
PT treating disorder associated with NF-kappaB activation e.g. cancer,
PT comprising amino acid sequence of human E3 ubiquitin ligase or its
variant.

XX Claim 1; Page 70-72; 77pp; English.

XX This is human E3 ubiquitin ligase (E3), which is homologous to human beta
CC -TrCP, an F-box/WD protein family member. E3 enhances ubiquitination of
CC phosphorylated I-kappa-B, an inhibitor protein of nuclear factor kappa-B
CC (NF-kappa-B). Understanding I-kappa-B degradation via the ubiquitin
CC pathway is useful for identifying modulators of this process for use in
CC treating diseases associated with activation of NF-kappa-B. In vitro

Qy 361 GHRAAVNVDFDDKYIVSASGDRITKMWSTSTCFVRLTNGHKGRIACLOVRDLVWSGS 420
Db 361 GHRAAVNVDFDDKYIVSASGDRITKMWSTSTCFVRLTNGHKGRIACLOVRDLVWSGS 420
Qy 421 SDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPA 480
Db 421 SDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPA 480
Qy 481 STLCLRTLVEHSGRVFRLQDFEQIISSSHDDTILIWDFLNVPPSAQNETSPTSRTYTYI 540
Db 481 STLCLRTLVEHSGRVFRLQDFEQIISSSHDDTILIWDFLNVPPSAQNETSPTSRTYTYI 540
Qy 541 SR 542
Db 541 SR 542
RESULT 3
AA040208
ID AA040208 standard; protein; 542 AA.
AC AA040208;
XX
22-OCT-2001 (first entry)
XX Human polypeptide SEQ ID NO 3353.
XX
XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokineic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
XX
XX 21-JAN-2000; 2000US-00488725.
XX
XX 25-APR-2000; 2000US-0052317.
XX
XX 20-JUN-2000; 2000US-00598042.
XX
XX 19-JUL-2000; 2000US-00620312.
XX
XX 03-AUG-2000; 2000US-00653450.
XX
XX 14-SEP-2000; 2000US-00662191.
XX
XX 19-OCT-2000; 2000US-00693036.
XX
XX 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX
XX N-PSDB; AA159364.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX Example 5; SEQ ID NO 3353; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AA038642-AA042213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 542 AA;
Query Match 100.0%; Score 2879; DB 4; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.8e-265;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEPSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCLOISNGTSSVIVS 60
Db 1 MEPSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCLOISNGTSSVIVS 60
Qy 61 RKRPSGNYQEKDLCIKYFDOWSESQDVEVEHLISRMCHYQHGHINSYLPKMLQORDFI 120
Db 61 RKRPSGNYQEKDLCIKYFDOWSESQDVEVEHLISRMCHYQHGHINSYLPKMLQORDFI 120
Qy 121 TALPEOGLDHTAENILSYLDARSLCAAEVLCCKEQRVISEGMLWKKLIERMVTRDPLWKG 180
Db 121 TALPEOGLDHTAENILSYLDARSLCAAEVLCCKEQRVISEGMLWKKLIERMVTRDPLWKG 180
Qy 181 LSERRGNDVLFKRPDTPGPNPFYRSLYPKIIODIETIESNWRGGRHNLQIOCRSENS 240
Db 181 LSERRGNDVLFKRPDTPGPNPFYRSLYPKIIODIETIESNWRGGRHNLQIOCRSENS 240
Qy 241 KGVYCLQYDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTSVLCLOYDERVIVTGSSDS 300
Db 241 KGVYCLQYDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTSVLCLOYDERVIVTGSSDS 300
Qy 301 TVRVMDVNTGEVLNLTLIHNEAVLHLRFSNGLMVTCSKDRSIAVMDMASATDITLRRVLV 360
Db 301 TVRVMDVNTGEVLNLTLIHNEAVLHLRFSNGLMVTCSKDRSIAVMDMASATDITLRRVLV 360
Qy 361 GHRAAVNVDFDDKYIVSASGDRITKMWSTSTCFVRLTNGHKGRIACLOVRDLVWSGS 420
Db 361 GHRAAVNVDFDDKYIVSASGDRITKMWSTSTCFVRLTNGHKGRIACLOVRDLVWSGS 420
Qy 421 SDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPA 480
Db 421 SDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPA 480
Qy 481 STLCLRTLVEHSGRVFRLQDFEQIISSSHDDTILIWDFLNVPPSAQNETSPTSRTYTYI 540
Db 481 STLCLRTLVEHSGRVFRLQDFEQIISSSHDDTILIWDFLNVPPSAQNETSPTSRTYTYI 540
Qy 541 SR 542
Db 541 SR 542
RESULT 4
ADS88293
ID ADS88293 standard; protein; 542 AA.
XX
XX ADS88293;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human protein of a TNF-alpha signalling pathway protein complex Seq 148.
XX
KW protein complex; tumour necrosis factor-alpha signalling pathway;
KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW inflammatory bowel disease; infectious disease; septic shock;
KW bacterial infection; neurological disease; stroke-induced inflammation;
KW neurodegenerative disease; cancer; antineoplastic; antidiabetic;
KW antirheumatic; cytostatic; antibacterial; gene therapy; human.
XX

CC short interfering RNA (siRNA) molecule. A method of reducing Cdc25A
CC degradation in a cell involves reducing beta-TrCP activity by reducing
CC the amount of beta-TrCP1 and/or TrCP2 in the cell e.g. by administering
CC an antisense or siRNA molecule. The methods, inhibitors, agents, and
CC compositions of the invention are useful for treating cancers, including
CC metastatic and primary cancers, and cancers characterized by solid or non
CC -solid tumors.

XX XX Sequence 542 AA;

Query Match 100.0%; Score 2879; DB 9; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.9e-265;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCIQISNGTSVVVS 60
Db 1 MEPSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCIQISNGTSVVVS 60
Qy 61 RRPSEGNQYQEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLPKMLQORDFI 120
Db 61 RRPSEGNQYQEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLPKMLQORDFI 120
Qy 121 TALPEQGLDHAENILSYLDARSLCAAEVLCKEQRVISEGMLWKLIERMVTRDPLWKG 180
Db 121 TALPEQGLDHAENILSYLDARSLCAAEVLCKEQRVISEGMLWKLIERMVTRDPLWKG 180
Qy 181 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIODIETIESNWRGCRHNLQRIQCRSENS 240
Db 181 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIODIETIESNWRGCRHNLQRIQCRSENS 240
Qy 241 KGVYCLQYDDDKIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVLCQYDERVIVTSSSDS 300
Db 241 KGVYCLQYDDDKIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVLCQYDERVIVTSSSDS 300
Qy 301 TVRVWDVNTGEVLNLIHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLV 360
Db 301 TVRVWDVNTGEVLNLIHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLV 360
Qy 361 GHRAAVNVDPDDKIIVSASGDRITIKWSTSTCFVRLTNGHKGICLQYDRDLVWGS 420
Db 361 GHRAAVNVDPDDKIIVSASGDRITIKWSTSTCFVRLTNGHKGICLQYDRDLVWGS 420
Qy 421 SDNTIRLWDIECGACLRVLEGEHELVRICIRFDNKRIVSGAYDGKIKWMDLQAALDPRA 480
Db 421 SDNTIRLWDIECGACLRVLEGEHELVRICIRFDNKRIVSGAYDGKIKWMDLQAALDPRA 480
Qy 481 STLCLRTLVEHSGRVFRLQDFEFOIISSSHDDTILWDFLNVPPSAQNETRSPRTYTI 540
Db 481 STLCLRTLVEHSGRVFRLQDFEFOIISSSHDDTILWDFLNVPPSAQNETRSPRTYTI 540
Qy 541 SR 542
Db 541 SR 542

RESULT 6
ID AAM41994 standard; protein; 550 AA.
XX XX
AC AAM41994;
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 6925.
XX XX
KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX', OS Homo, sapiens.

XX WO200153312-A1.
PN 26-JUL-2001.
PD 26-DEC-2000; 2000WO-US034263.
XX 23-DEC-1999; 99US-004711275.
XX 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX (HYSE-) HYSEQ INC.
FA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
PI WPI; 2001-442253/47.
XX DR N-PSDB; AAI61150.
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
PT Example 2; SEQ ID NO 6925; 10078pp; English.
PS The invention relates to human nucleic acids (AAI57798-AAI61369) and the
XX encoded polypeptides (AAM38642-AAM42213) with nontropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX SQ Sequence 550 AA;
Query Match 100.0%; Score 2879; DB 4; Length 550;
Best Local Similarity 100.0%; Pred. No. 2.9e-265;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEPSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCIQISNGTSVVVS 60
Db 9 MEPSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCIQISNGTSVVVS 68
Qy 61 RRPSEGNQYQEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLPKMLQORDFI 120
Db 69 RRPSEGNQYQEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLPKMLQORDFI 128
Qy 121 TALPEQGLDHAENILSYLDARSLCAAEVLCKEQRVISEGMLWKLIERMVTRDPLWKG 180
Db 129 TALPEQGLDHAENILSYLDARSLCAAEVLCKEQRVISEGMLWKLIERMVTRDPLWKG 188
Qy 181 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIODIETIESNWRGCRHNLQRIQCRSENS 240
Db 189 LSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIODIETIESNWRGCRHNLQRIQCRSENS 248
Qy 241 KGVYCLQYDDDKIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVLCQYDERVIVTSSSDS 300
Db 249 KGVYCLQYDDDKIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVLCQYDERVIVTSSSDS 308

QY 301 TVRVWDVNTGEVLNTLIHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRLVLV 360
 DB 309 TVRVWDVNTGEVLNTLIHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRLVLV 368
 QY 361 GHRAAVNVVDFDDKYIVSASGDRTIKVMSTSTCEVFTLNGHKGRIACIQYRDLRVVSGS 420
 DB 369 GHRAAVNVVDFDDKYIVSASGDRTIKVMSTSTCEVFTLNGHKGRIACIQYRDLRVVSGS 428
 QY 421 SDNTIRLWDIECGACLRVLEGGHEELVRCIRFNDKNRIVSGAYDGKIIVWDLQAALDPRAPA 480
 DB 429 SDNTIRLWDIECGACLRVLEGGHEELVRCIRFNDKNRIVSGAYDGKIIVWDLQAALDPRAPA 488
 QY 481 STLCLRTLVEHSGRVRFLQDFEQIISSSHDDTILWDFLNVPPSAQNETRSRPTTYI 540
 DB 489 STLCLRTLVEHSGRVRFLQDFEQIISSSHDDTILWDFLNVPPSAQNETRSRPTTYI 548
 QY 541 SR 542
 DB 549 SR 550

RESULT 7
 ADX05977
 ID ADX05977 standard; protein; 542 AA.
 AC ADX05977;
 XX
 XX
 XX 21-APR-2005 (first entry)
 XX
 XX Cyclin-dependent kinase modulation biomarker SEQ ID NO 542.
 XX
 XX cytostatic; cyclin-dependent kinase; cdk; biomarker.
 XX
 XX Homo sapiens.
 XX
 XX HQ2005012875-A2.
 XX
 XX 10-FEB-2005.
 XX
 XX 29-JUL-2004; 2004WO-US024424.
 XX
 XX 29-JUL-2003; 2003US-0490890P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
 PI
 DR WPI; 2005-163068/17.
 DR N-PSDB; ADX05976.
 XX

XX Biomarkers useful for predicting or determining the response of a mammal
 PT to a cancer treatment comprising administration of a modulator of cyclin-
 PT dependent kinase activity.
 XX

PS Claim 5; SEQ ID NO 542; 141pp; English.

XX This invention describes a novel method of predicting or determining
 CC whether a mammal will respond or is responding to an anti-cancer agent
 CC that modulates cyclin-dependent kinase (cdk) activity. The method
 CC comprises measuring the level of one or more biomarkers selected from
 CC 2174 biomarkers given in the specification (nucleotide sequence SEQ ID
 CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
 CC invention is utilized in a kit for determining or predicting whether
 CC patient would be susceptible or resistant to treatment by an agent
 CC modulating cdk activity. The invention also describes a method for
 CC utilizing individualized genetic profiles for treating diseases and
 CC disorders based on patient's response and molecular level, specialized
 CC microarrays comprising the biomarkers described, antibodies directed
 CC against the biomarkers and a cell culture model to identify biomarkers.
 CC The cdk modulator is preferably N-5-[(5-(1,1-dimethylethyl))-2-
 CC oxazolyl]methylthio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
 CC tartaric acid salt. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published pct sequences. This
 CC sequence represents a biomarker used in the method of the invention.
 XX
 XX Sequence 542 AA;

Query Match 99.8%; Score 2873; DB 9; Length 542;
 Best Local Similarity 99.8%; Pred. No. 1e-264; Mismatches 1; Indels 0; Gaps 0;
 Matches 541; Conservative 0;

QY 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCLOISNGTSSVIVS 60
 DB 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCLOISNGTSSVIVS 60
 QY 61 RRPSEGNVQKEDKCIKYFDQWSSDQVEFVEHLISRMCHYOHGHINLYLKPMLORDFI 120
 DB 61 RRPSEGNVQKEDKCIKYFDQWSSDQVEFVEHLISRMCHYOHGHINLYLKPMLORDFI 120
 QY 121 TALPEQGLDHIENILSYLDARSLCAELVCKEQRVISEGMLWKKLIERMVTRDPLWKG 180
 DB 121 TALPEQGLDHIENILSYLDARSLCAELVCKEQRVISEGMLWKKLIERMVTRDPLWKG 180
 QY 181 LSEREGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNWRGCRHNLQRIQCRSENS 240
 DB 181 LSEREGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNWRGCRHNLQRIQCRSENS 240
 QY 241 KGVYCLQYDDEKIIISGLRDNISIKINDKTSLECLKVLTGHTGSLVLCLOYDERVIVTSSDS 300
 DB 241 KGVYCLQYDDEKIIISGLRDNISIKINDKTSLECLKVLTGHTGSLVLCLOYDERVIVTSSDS 300
 QY 301 TVRVWDVNTGEVLNTLIHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRLVLV 360
 DB 301 TVRVWDVNTGEVLNTLIHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRLVLV 360
 QY 361 GHRAAVNVVDFDDKYIVSASGDRTIKVMSTSTCEVFTLNGHKGRIACIQYRDLRVVSGS 420
 DB 361 GHRAAVNVVDFDDKYIVSASGDRTIKVMSTSTCEVFTLNGHKGRIACIQYRDLRVVSGS 420
 QY 421 SDNTIRLWDIECGACLRVLEGGHEELVRCIRFNDKNRIVSGAYDGKIIVWDLQAALDPRAPA 480
 DB 421 SDNTIRLWDIECGACLRVLEGGHEELVRCIRFNDKNRIVSGAYDGKIIVWDLQAALDPRAPA 480
 QY 481 STLCLRTLVEHSGRVRFLQDFEQIISSSHDDTILWDFLNVPPSAQNETRSRPTTYI 540
 DB 481 STLCLRTLVEHSGRVRFLQDFEQIISSSHDDTILWDFLNVPPSAQNETRSRPTTYI 540
 QY 541 SR 542
 DB 541 SR 542

RESULT 8
 ADX88282
 ID ADX88282 standard; protein; 563 AA.
 XX
 XX ADX88282;
 AC
 XX

18-NOV-2004 (first entry)

Human protein of a TNF-alpha signalling pathway protein complex Seq 137.
 protein complex; tumour necrosis factor-alpha signalling pathway;
 TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
 inflammatory bowel disease; infectious disease; septic shock;
 bacterial infection; neurological disease; stroke-induced inflammation;
 neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
 antirheumatic; cytostatic; antibacterial; gene therapy; human.
 XX Homo sapiens.
 OS
 XX WO2004035783-A2.
 PN
 XX 29-APR-2004.
 PD
 XX

PF 24-SEP-2003; 2003WO-EP050655.
XX
PR 26-SEP-2002; 2002EP-00021809.
PR 10-FEB-2003; 2003EP-00100274.
XX
XX (CELL-) CELLZOME AG.
XX
XX Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
PI Superti-Furga G, Kruse U;
PI
XX WPI; 2004-348460/32.
XX
XX
PT New protein complex comprising at least one first and second protein of
PT the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
PT diagnosing or treating inflammation, neurological diseases, infectious
PT diseases or cancer.
XX
XX Example; SEQ ID NO 137; 1980pp; English.
XX
XX This invention relates to novel protein complexes of the tumour necrosis
XX factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
XX methods for preparing these complexes comprising at least two component
XX proteins, as well as screening methods to identify modulators of the
XX pathway, which include antibodies, agonists and antagonists thereof. The
XX present invention describes a protein complex and kit that are useful for
XX diagnosing, prognosing or treating chronic inflammatory diseases such as
XX rheumatoid arthritis and inflammatory bowel disease; infectious diseases
XX such as septic shock and bacterial infections; neurological diseases such
XX as stroke-induced inflammation in neurons; neurodegenerative diseases and
XX cancer. Accordingly, these complexes can be used for the development of
XX pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
XX antirheumatic, cytostatic and antibacterial activities and can be used
XX for gene therapy purposes. In particular, the invention further provides
XX siRNA-oligonucleotides useful for inhibiting protein expression for in
XX vitro or cell culture assays. This polypeptide is a human protein that
XX can be used in combination with other proteins provided in the
XX specification to form novel complexes of the TNF-alpha signalling pathway
XX of the invention.
XX
XX Sequence 563 AA;
XX
Query Match 95.7%; Score 2755.5; DB 8; Length 563;
Best Local Similarity 93.3%; Pred. No. 1.8e-253;
Matches 525; Conservative 2; Mismatches 15; Indels 21; Gaps 1;
QY 1 MEPSDVIEDKTIELMCSVPRSLMIGCANLVESMCALSCLOSMPSVRCL----- 48
DB 1 MEPSDVIEDKTIELMCSVPRSLMIGCANLVESMCALSCLOSMPSVRCLQNTSVMEDQNE 60
QY 49 -----QISNGTSSVIVSRKPSGNYQKEKDLCKYFDOWSESDQVEFVHLLSRM 99
DB 61 ESPKKSALWQISNGTSSVIVSRKPSGNYQKEKDLCKYFDOWSESDQVEFVHLLSRM 120
QY 100 CHYQHGHSYLPKMLQRFITALPEQGLDHAENILSYLDARSCLAAELVCKEWRVIS 159
DB 121 CHYQHGHSYLPKMLQRFITALPEQGLDHAENILSYLDARSCLAAELVCKEWRVIS 180
QY 160 EGMWLKLIERWVRTDPLWKLSERRGWQYLFKNRPTDGPNSFYRSPLPKIIDIETI 219
DB 181 EGMWLKLIERWVRTDPLWKLSERRGWQYLFKNRPTDGPNSFYRSPLPKIIDIETI 240
QY 220 ESNWRCGRHNLQRIQCSSENSKVYCYLOYDDEKILSGLRDNSIKWPKTSLECLKVLVTH 279
DB 241 ESNWRCGRHNLQRIQCSSENSKVYCYLOYDDEKILSGLRDNSIKWPKTSLECLKVLVTH 300
QY 280 TGSVLCLOYDERIVITGSSDSTVRVMDVNTGEVLTILHNEAVLHFRFNGMLVTCSD 339
DB 301 TGSVLCLOYDERIVITGSSDSTVRVMDVNTGEVLTILHNEAVLHFRFNGMLVTCSD 360
QY 340 RSIADVMDASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWSTSTCEFVRTL 399
DB 361 RSIADVMDAFCHRYHFFPCSGWPRAAVNVVDFDDKYIVSASGDRITIKWSTSTCEFVRTL 420

400 NGHKRGIAQLQYRDRLVWVGSSDNTIRLWDIEGACLRVLEGHLEELVRCIRFDFNKRIVSG 459
DB 421 NGHKRGIAQLQYRDRLVWVGSSDNTIRLWDIEGACLRVLEGHLEELVRCIRFDFNKRIVSG 480
QY 460 AYDGKIKVWDLOAALDPRAPASTLCRLTLVEHSGRVFRLQDFDFQIISSSHDDTILWDF 519
DB 481 AYDGKIKVWDLOAALDPRAPASTLCRLTLVEHSGRVFRLQDFDFQIISSSHDDTILWDF 540
QY 520 LNVPPSAQNETRSPSRITYIYSR 542
DB 541 LNVPPSAQNETRSPFRITYIYSR 563

RESULT 9
ADX05979
ID ADX05979 standard; protein; 529 AA.
XX
AC ADX05979;
XX
DT 21-APR-2005 (first entry)
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 544.
XX
XX cytosstatic; cyclin-dependent kinase; cdk; biomarker.
XX
OS Homo sapiens.
XX
PN W02005012875-A2.
XX
PD 10-FEB-2005.
XX
PF 29-JUL-2004; 2004WO-US024424.
XX
PR 29-JUL-2003; 2003US-0490890P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
DR WPI; 2005-163068/17.
DR N-PSDB; ADX05978.
XX
XX Biomarkers useful for predicting or determining the response of a mammal
XX to a cancer treatment comprising administration of a modulator of cyclin-
XX dependent kinase activity.
XX
PS Claim 5; SEQ ID NO 544; 141pp; English.
XX
XX This invention describes a novel method of predicting or determining
XX whether a mammal will respond or is responding to an anti-cancer agent
XX that modulates cyclin-dependent kinase (cdk) activity. The method
XX comprises measuring the level of one or more biomarkers selected from
XX 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
XX NO:1246 (Genbank EST W28729) is especially preferred). The method of the
XX invention is utilized in a kit for determining or predicting whether
XX patient would be susceptible or resistant to treatment by an agent
XX modulating cdk activity. The invention also describes a method for
XX utilizing individualized genetic profiles for treating diseases and
XX disorders based on patient's response and molecular level, specialized
XX microarrays comprising the biomarkers described, antibodies directed
XX against the biomarkers and a cell culture model to identify biomarkers.
XX The cdk modulator is preferably N-5-[(5-(1,1-Dimethylethyl)-2-
XX oxazolyl)methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
XX tartaric acid salt. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
XX sequence represents a biomarker used in the method of the invention.
XX
SQ Sequence 529 AA;
Query Match 92.6%; Score 2666.5; DB 9; Length 529;
Best Local Similarity 92.4%; Pred. No. 5.2e-245;
Matches 512; Conservative 1; Mismatches 4; Indels 37; Gaps 3;

Qy	1	MEPDSVIEDKTIELM-CSV-----PRSLWLGCANLVESMCALSCLOSMPSVRCL	48
Db	1	MEPDSVIEDKTIELMNTSVMEDQNEDESPPKNTLW-----	35
Qy	49	QISNGTSSVIVSRKRPSEGNQYQEKDKLCIKYFDQWSESQVEFVBEHLISRMCHYQHGHN	108
Db	36	QISNGTSSVIVSRKRPSEGNQYQEKDKLCIKYFDQWSESQVEFVBEHLISRMCHYQHGHN	95
Qy	109	SYLXPMQLORDFITALPEOGLDHIABENILSYLDARSLCAAEVLCCKEQRVISEGMLWKKLI	168
Db	96	SYLXPMQLORDFITALPEOGLDHIABENILSYLDARSLCAAEVLCCKEQRVISEGMLWKKLI	155
Qy	169	ERMVRTDPLWKGLESRRGWDQVLFKNRPTDGPNSFYRSLYPKIIQDIETIESNWRCCGRH	228
Db	156	ERMVRTDPLWKGLESRRGWDQVLFKNRPTDGPNSFYRSLYPKIIQDIETIESNWRCCGRH	215
Qy	229	NLQRIQCRSENSKGVCYLQYDDEKIIISGLRDNSIKIWDKTSLECLKVLTGHTGSLCQY	288
Db	216	NLQRIQCRSENSKGVCYLQYDDEKIIISGLRDNSIKIWDKTSLECLKVLTGHTGSLCQY	275
Qy	289	DERVIVTGSSDSTRVRVDNVTGVEVNTLIIHNEAVLHLRFSNGLMVTCSKDRSIAWDMVA	348
Db	276	DERVIVTGSSDSTRVRVDNVTGVEVNTLIIHNEAVLHLRFSNGLMVTCSKDRSIAWDMVA	335
Qy	349	SATDITILRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKWSTSTCEFVRTLNGHKRGIA	408
Db	336	SATDITILRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKWSTSTCEFVRTLNGHKRGIA	395
Qy	409	LOYRDLRVSSGSDNTIRLWDIECCGACLRVLGHEELVRCIRFDNKRIVSGAYDGKIKW	468
Db	396	LOYRDLRVSSGSDNTIRLWDIECCGACLRVLGHEELVRCIRFDNKRIVSGAYDGKIKW	455
Qy	469	DLQAALDPRAPASTLCLRTLVEHSGRVRFLQDFEQIISSSHDDTILIWDFLNVPPSAQN	528
Db	456	DLQAALDPRAPASTLCLRTLVEHSGRVRFLQDFEQIISSSHDDTILIWDFLNVPPSAQN	515
Qy	529	ETRSPSRITYTIVSR	542
Db	516	ETRSPSRITYTIVSR	529

RESULT 10
ADX05981
ID ADX05981 standard: protein: 508 AA.

ADX05981;
21-APR-2005 (first entry)

Cyclin-dependent kinase modulation biomarker SEQ ID NO 546.

OS Homo sapiens.

PN WO2005012875-A2.

PD 10-FEB-2005.

PF 29-JUL-2004; 2004WO-US024424.

PR 29-JUL-2003; 2003US-0490890P.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;

DR WPI; 2005-163068/17.

XX
PT

...PT to a cancer treatment comprising administration of a modulator of cyclin-

dependent kinase activity.

Claim 5; SEQ ID NO 546; 141pp; English.

This invention describes a novel method of predicting or determining whether a mammal will respond or is responding to an anti-cancer agent that modulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more biomarkers selected from 2774 biomarkers given in the specification (nucleotide sequence SEQ ID NO:1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers.

The cdk modulator is preferably N-5-[(5-(1,1-Dimethylethyl)-2-oxazolyl)methyl]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-tartaric acid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct_sequences. This sequence represents a biomarker used in the method of the invention.

Sequence 508 AA;

Query Match	92.4%	Score 2661;	DB 9;	Length 508;
Best Local Similarity	93.5%;	Pred. No. 1.6e-244;		
Matches 507; Conservative	0;	Mismatches 1;	Indels 34;	Gaps 1;

Qy	1	MEPDSVIEDKTIELMCSVPSRLWGLCANLVESMCALSCLOMPSVRCLOJISNGTSSVVIS	60
Db	1	MEPDSVIEDKTIELM-----ISNGTSSVVIS	26
Qy	61	RKRPSEGNQKEXDLCKIYFDQWSESDQVEFVHILSRMCHYQGHINSYLKPMQLORDFI	120
Db	27	RKRPSEGNQKEXDLCKIYFDQWSESDQVEFVHILSRMCHYQGHINSYLKPMQLORDFI	86
Qy	121	TALPEQGLDHHAEINILSYLDARSLCAELVCKEHWVISEGMLWKKLIEMVRTDPLWKG	180

Qy	181	LSERRGWDQVLFKNRPDTGPPNSFYRSLYPKIIQDIETIESNWRCGRHNLIQRIQCRSENS	241
Db	147	LSESRGWDQVLFKNRPDTGPPNSFYRSLYPKIIQDIETIESNWRCGRHNLIQRIQCRSENS	206
Qy	241	KGVCLOYDDKEIKISGLRDNSIKIWDKTSLECLKVLFGHTGSVLCLOYDERVIVTGSDDS	300
Db	207	KGVCLOYDDKEIKISGLRDNSIKIWDKTSLECLKVLFGHTGSVLCLOYDERVIVTGSDDS	266
Qy	301	TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMWTCCKDRSIAVMDWASATDITLRRVLV	360
Db	267	TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMWTCCKDRSIAVMDWASATDITLRRVLV	326
Qy	361	GHRAAVNVVDFDDKIIVSASGDRTIKVMWSTSTCEBFTLNGHKRGIAQLOYRDRDLVVSGS	420
Db	327	GHRAAVNVVDFDDKIIVSASGDRTIKVMWSTSTCEBFTLNGHKRGIAQLOYRDRDLVVSGS	386
Qy	421	SDNTIRLWDECGACLRLVSGHEELVRCIRFDNKRIVSGAYDGRIKVMWDLQAALDPRAPA	480
Db	387	SDNTIRLWDECGACLRLVSGHEELVRCIRFDNKRIVSGAYDGRIKVMWDLQAALDPRAPA	446
Qy	481	STLCRLTLVEHSGRVFLQDFEFOIISSSHDDTTILIWDFLNVPPSAQNETRSPSRTYTI	540
Db	447	STLCRLTLVEHSGRVFLQDFEFOIISSSHDDTTILIWDFLNVPPSAQNETRSPSRTYTI	506
Qy	541	SR	542
Db	507	SR	508

RESULT 11
AAM78583

DB	121	SDQVEFVEHLISQCHYQHGHSYLPKMLQDFITALPARGLDHPHIAENILSYLDAKSLC	180
QY	146	AELVCKEWRVISEGMLWKKLIERMYRTDPLWKLSEBRCWDOYLFKNRPTDG--PPNS	203
DB	181	AELVCKEWRVITSDGMLWKKLIERMYRTDPLWKLSEBRCWDOYLFKNRPTDG--PPNS	240
QY	204	FYRSLYPKIITQDIETIESNRWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIIISGLRDSIK	263
DB	241	FYRALYPKIITQDIETIESNRWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIIISGLRDSIK	300
QY	264	IWKTSLECKVLVTGHTGSLVCLQYDERVITGSSDSTVRVWVNTGEVLTNLHNEAV	323
DB	301	IWKNTLECKRIITGHTGSLVCLQYDERVITGSSDSTVRVWVNTGEVLTNLHNEAV	360
QY	324	LHLRFSNGLMVTCKORSIAVWDMASATDITLRLVVGRAAANNVDFDDKIIVSASGDR	383
DB	361	LHLRFNNGMMVTCKORSIAVWDMASPTDITLRLVVGRAAANNVDFDDKIIVSASGDR	420
QY	384	TIKWTSTCEVFRTLNHKGRIACQYRDLRVVSGSSDNTIRLWDIECGACLRVLEGHE	443
DB	421	TIKWTSTCEVFRTLNHKGRIACQYRDLRVVSGSSDNTIRLWDIECGACLRVLEGHE	480
QY	444	ELVRCIRFDNKRIVSGAYDGKIKVWDLQALDPRAPASTLCRLTLVHSGRVFRLQDFEF	503
DB	481	ELVRCIRFDNKRIVSGAYDGKIKVWDLVAAALDPRAPAGTLCRLTLVHSGRVFRLQDFEF	540
QY	504	QIITSSSHDDTILWDLNVPVPSAQNETRSPSRVTYIISR	542
DB	541	QIVSSSHDDTILWDLNVPVPSAQNETRSPSRVTYIISR	579
RESULT 12			
AAAM78582	ID	AAAM78582 standard; protein; 605 AA.	
XX	AC	AAAM78582;	
XX	DT	06-NOV-2001 (first entry)	
XX	DE	Human protein SEQ ID NO 1244.	
XX	KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;	
XX	KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;	
XX	KW	tissue growth factor; immunomodulatory; cancer; leukaemia;	
XX	KW	nervous system disorder; arthritis; inflammation.	
XX	OS	Homo sapiens.	
XX	PN	WO200157190-A2.	
XX	PD	09-AUG-2001.	
XX	PR	05-FEB-2001; 2001WO-US004098.	
XX	PR	03-FEB-2000; 2000US-00496914.	
XX	PR	27-APR-2000; 2000US-00560875.	
XX	PR	20-JUN-2000; 2000US-00598075.	
XX	PR	19-JUL-2000; 2000US-00620325.	
XX	PR	01-SEP-2000; 2000US-00654936.	
XX	PR	15-SEP-2000; 2000US-00663561.	
XX	PR	20-OCT-2000; 2000US-00693325.	
XX	PR	30-NOV-2000; 2000US-00728422.	
XX	PA	(HYSE-) HYSEQ INC.	
XX	PI	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;	
XX	PI	Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;	
XX	PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R;	
XX	XX	WPI; 2001-476283/51.	
XX	XX	N-PSDB; AAK51715.	

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.

PS Claim 20; Page 3503-3504; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM90302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication

XX Sequence 605 AA;

Query Match 84.9%; Score 2445.5; DB 4; Length 605;
Best Local Similarity 75.7%; Pred. No. 8e-224;
Matches 458; Conservative 49; Mismatches 35; Indels 63; Gaps 4;

QY 1 MEP-DSVIEDKTIELMCSVPRSLWLGCSLADSMPSLRCLYNPGTGALTAFMNSSREDC 39

Db 1 MDPAAEVLQEKALKFMCSPRSLWLGCSLADSMPSLRCLYNPGTGALTAFMNSSREDC 60

QY 40 -----QSMPSVRCL---QISNGTSSVIV 59

Db 61 NNGEPPRKIIPEKNSLRQTVNSCARLCLNQETVCLASTAMKTCNCVAKTKLANGTSSMIV 120

QY 60 SRKPSGNYQKEDLCIKYFDOWSESDQVEFVHILISRMCHYQHGHINSYLPKMLQRDF 119

Db 121 PKQKLSASVEKEKELCVKFEQWSESDQVEFVHILISQCHYQHGHINSYLPKMLQRDF 180

QY 120 ITALPEGLDHIATNLSYLDARSLCAAEVLCKEAWORVISEGMLWKKLIERMVTRDPLWK 179

Db 181 ITALPARGLDHIAENILSYLDKSLCAAEVLCKEAWRVVTSQGLWKKLIERMVTRDSLWR 240

QY 180 GLSERGWDQYLFKNRPTDG--PPNSFYRSLYPKIIDIETIESNNRCGRHNLQRCRS 237

Db 241 GLAERRGWGQYLFKNRPPDGNAPPNSFYRALYPKIIDIETIESNNRCGRHSLQRIHCRS 300

QY 238 ENSKGVVCLQYDDKEIISGLRDSIKIWDKTSLECLKVLGTGHTGSLCLQYDERVIVTGS 297

Db 301 ETSKGVVCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILLTGTGSLCLQYDERVIVTGS 360

QY 298 SDSTVRVMDVNTGEVMTLIIHNEAVLHFRSGLMVTCSDKRSIAVWDMASATDITLRR 357

Db 361 SDSTVRVMDVNTGEVMTLIIHCEAVLHFRFNGMVMVTCSDKRSIAVWDMASATDITLRR 420

QY 358 VLVGHRAAVNVDPDDKIVYASGDRTIKVMSTSTCFVFTLNCHKRGIAICLQYRDLVV 417

Db 421 VLVGHRAAVNVDPDDKIVYASGDRTIKVMWNTSTCFVFTLNCHKRGIAICLQYRDLVV 480

QY 418 SGSSDNTIRLWDIECGACLVLEGHEELVRCIRFDNKRIVSGAYDGRKIVWDIQAALDPR 477

Db 481 SGSSDNTIRLWDIECGACLVLEGHEELVRCIRFDNKRIVSGAYDGRKIVWDIQAALDPR 540

QY 478 APASTLCRLTVEHSGRVFRQLQDFEQIISSHDDTTILWDFLNVPSPAQNETRSPRTY 537

Db 541 APAGTLCRLTVEHSGRVFRQLQDFEQIVSSSHDDTTILWDFLNPAQAAPRPSRPT 600

QY 538 TYISR 542

Db 601 TYISR 605

RESULT 13

ADS88274

ID ADS88274 standard; protein; 605 AA.

XX

AC ADS88274;

DT 18-NOV-2004 (first entry)

DE

XX Human protein of a TNF-alpha signalling pathway protein complex Seq 129.
DE protein complex; tumour necrosis factor-alpha signalling pathway;
XX TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW inflammatory bowel disease; infectious disease; septic shock;
KW bacterial infection; neurological disease; stroke-induced inflammation;
KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
KW antirheumatic; cytostatic; antibacterial; gene therapy; human.

XX Homo sapiens.

OS WO2004035783-A2.

PN 29-APR-2004.

XX 24-SEP-2003; 2003WO-EP050655.

PF 26-SEP-2002; 2002EP-00021809.

PR 10-FEB-2003; 2003EP-00100274.

XX (CELL-) CELLZONE AG.

PA Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
PI Superti-Furga G, Kruse U;
XX WPI; 2004-348460/32.

DR

XX New protein complex comprising at least one first and second protein of
PT the Tumor Necrosis Factor-alpha (TNF-alpha)-signaling pathway, useful for
PT diagnosing or treating inflammation, neurological diseases, infectious
PT diseases or cancer.

XX Example; SEQ ID NO 129; 1980pp; English.

PS This invention relates to novel protein complexes of the tumour necrosis
XX factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
CC methods for preparing these complexes comprising at least two component
CC proteins, as well as screening methods to identify modulators of the
CC pathway, which include antibodies, agonists and antagonists thereof. The
CC present invention describes a protein complex and kit that are useful for
CC diagnosing, prognosing or treating chronic inflammatory diseases such as
CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
CC such as septic shock and bacterial infections; neurological diseases such
CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC cancer. Accordingly, these complexes can be used for the development of
CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
CC antirheumatic, cytostatic and antibacterial activities and can be used
CC for gene therapy purposes. In particular, the invention further provides
CC siRNA-oligonucleotides useful for inhibiting protein expression for in
CC vitro or cell culture assays. This polypeptide is a human protein that
CC can be used in combination with other proteins provided in the
CC specification to form novel complexes of the TNF-alpha signalling pathway
CC of the invention.

XX Sequence 605 AA;

Query Match 84.9%; Score 2445.5; DB 8; Length 605;

Best Local Similarity 75.7%; Pred. No. 8e-224;

Matches 458; Conservative 49; Mismatches 35; Indels 63; Gaps 4;

QY 1 MEP-DSVIEDKTIELMCSVPRSLWLGCSLADSMPSLRCLYNPGTGALTAFONSSREDC 39

Db 1 MDPAAEVLQEKALKFMCSPRSLWLGCSLADSMPSLRCLYNPGTGALTAFONSSREDC 60

QY 40 -----QSMPSVRCL---QISNGTSSVIV 59

Db 61 NNGEPPRKIIPEKNSLRQTVNSCARLCLNQETVCLASTAMKTCNCVAKTKLANGTSSMIV 120

Query Match	84.2%	Score 2423	DB 4	Length 654
Best Local Similarity	72.5%	Pred. No. 1.3e-21		
Matches 458	Conservative 49	Mismatches 35	Indels 90	Gaps 5
Qv 1	MEP-DSVIEDKTIELM	-----CSVPSRLWLGCA	LVES 32	
	: : : : :	: : : : :		
Db 23	MDPAEAVLQEKALFEMFE	RSWCPCGWNMTARS	LTATSTRVQCSPMPSRLW	LGCS
				SLADS 82
Qv 33	MCALSCSL	-----		39

PI^a Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 25, 2006, 07:17:37 ; Search time 41 Seconds
(without alignments)
1271.939 Million cell updates/sec

Title: US-10-665-715-16

Perfect score: 2879

Sequence: 1 MEPDSVIEDKTIELMCSVPR.....PPSAQNTRSPSRTYIISR 542

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2301	79.9	518	B48088	beta-transducin re
2	1638.5	56.9	701	T18607	hypothetical prote
3	683.5	23.7	506	T50211	WD-repeat protei
4	584	20.3	605	T38932	probable sulfur me
5	538	18.7	640	S49932	MET30 protein - ye
6	525	18.2	650	T46660	sulfur controller-
7	516.5	17.9	267	S62507	hypothetical trp-a
8	512	17.8	579	T22703	hypothetical prote
9	468.5	16.3	1356	T18521	beta transducin-l1
10	453	15.7	775	T45136	WD repeat protei
11	425	14.8	1227	AE1810	WD-40 repeat prote
12	418	14.5	779	S56245	cell division cont
13	389.5	13.5	703	T43557	F-box/WD-repeat pr
14	387.5	13.5	1189	A12493	WD-repeat protei
15	383.5	13.3	1747	AC1842	WD-40 repeat prote
16	378.5	13.1	1258	A12155	WD-repeat protei
17	377.5	13.1	1526	AC2329	WD-40 repeat prote
18	374	13.0	1683	AF7071	WD-40 repeat prote
19	360.5	12.5	677	AE1861	serine/threonine k
20	359.5	12.5	559	AB2202	hypothetical prote
21	347	12.1	1711	AD1842	WD-40 repeat prote
22	343	11.9	409	S36113	LIS-1 protein - hu
23	343	11.9	410	S48052	platelet-activatin
24	343	11.9	1146	A55532	myosin-heavy-chain
25	340.5	11.8	777	T41075	hypothetical WD-re
26	340	11.8	515	S19487	hypothetical prote
27	339	11.8	676	AH2195	hypothetical prote
28	329.5	11.4	317	T46032	WD-40 repeat regul
29	323	11.2	333	G85034	probable WD-repeat

RESULT 1

B48088

beta-transducin repeat-containing protein - African clawed frog

N:Alternate names: beta-Trcp

C:Species: Xenopus laevis (African clawed frog)

C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C:Accession: B48088

R:Spievak, W.; Keiper, B.D.; Stratowa, C.; Castanon, M.J.

Mol. Cell. Biol. 13, 4953-4966, 1993

A:Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase arr

A:Reference number: A48088; MUID:93330289; PMID:8393141

A:Accession: B48088

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-518 <SP>

A:Cross-references: UNIPROT:Q91854; UNIPARC:UPI0000137338; GB:M98268; NID:G295542; PIDN

C:Keywords: duplication

F:431-462/Domain: WD repeat homology <WD1>

Query Match 79.9%; Score 2301; DB 2; Length 518;

Best Local Similarity 88.0%; Pred. No. 1.9e-166;

Matches 424; Conservative 33; Mismatches 23; Indels 2; Gaps 1;

QY	44	SVRCIQISNGTSSVTVSRKRPSEGNVQKEKDLCKYFDQWSESDQVFEVHILSRMCHYQ	103
DB	34	TLRQTKLANGSSMIVPKQKLSANYEKEKELCVKIFQWSECDQVFEVHILSRMCHYQ	93
QY	104	HGHINSYLPKMLQRFITALPEQGLDHAENILSYLDARSLSAELVCKEWMORVISEGML	163
DB	94	HGHINTYLPKMLQRFITALPARGLDHAENILSYLDAKSLCSAELVCKEWMRVVTSQGL	153
QY	164	WKKLIERMVRTDPLWKGLSERGWQYLFKQRPDTG--PPNSFYRSLVPKIIQDIETIES	221
DB	154	WKKLIERMVRTDSLWRGLAERRGWQYLFKNKPPDGKTPPNISFYRSLVPKIIQDIETIES	213
QY	222	NWRCGRHNLRIQCHSENSKGVYCLQYDDEKIIISGLRNSIKWDKTSLECLKVLGTHTG	281
DB	214	NWRCGRHSLRIQCHSETSKGVYCLQYDQDKIVSGVRDNTIKWDKNTLECKRVLMGHTG	273
QY	282	SVLCIQYDERVITGSSDSTVRVMDVNTGEVLNTLIHNEAVLHLRFNSGLMVTCKORS	341
DB	274	SVLCIQYDERVITGSSDSTVRVMDVNTGEVLNTLIHNEAVLHLRFNNGMVTCKORS	333
QY	342	IAVMDASATDITLRVLVGHRAAVNVVDQDKYIVSASGDRITIKVNSTSTCEPVRTLNG	401
DB	334	IAVMDASATDITLRVLVGHRAAVNVVDQDKYIVSASGDRITIKVNSTSTCEPVRTLNG	393
QY	402	HKRGACIQYDRDLVVGSSDNTIRLWDIECGACLRVLEEGHEELVRCIRFDNKRIVSGAY	461
DB	394	HKRGACIQYDRDLVVGSSDNTIRLWDIECGACLRVLEEGHEELVRCIRFDNKRIVSGAY	453
QY	462	DGKIKVQDLQAALDPRAPASTLCRLTLVEHSGRVPRQLQFDFEQIITSSSHDDTLILWDFLN	521

Qy 62 KRSEGN-----YQEKDL--CIKVPDQWSESQQVEFVHILSRMCHYQHGHINSYLK 112
 |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
 Db 117 KRTQEINANTAKLPQBCSDIHIIISKYSNSNDKIRKLILDGILLSTSCFPQLSYSSIVLT 176
 Qy 113 PMLQRDPITALPEGLDHIAENILSYLDARSLCAAEIACKEWQRVISGMLWKLIERMV 172
 |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
 Db 177 HMKIDIFISLPB---LSLKILSYLDCQLCLNATRCRKQKLADDDRVVYWHCEQHI 232
 Qy 173 RTDPLMWKGLSERR----GWDOYLFKNR-----PTDGPSPNFYSRLY 209
 :|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
 Db 233 -----DRKCPNGCWGLPLLHMKRARIQNOSTSGSSNADIQTQTRPWKVYRRERF 282
 Qy 210 PKIIDTETTESWRGRHNLRIOCRSENSK----GVYCLOYDDEKIISGLRDSIKIW 265
 :|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
 Db 283 -----KVESNNRWKG-----HCRIQEFKGMHDGVLTLQFNRYLLFTGSYDSTIGIW 327
 Qy 266 DKTSLECLKVLTGHTSGVLCLOYDERVILVTGSSDSTRVRVDVNTGEVINTLIHHNEAVLH 325
 :||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
 Db 328 DLFTGKLIIRLSHGSHDGKTYLFDRLKLTGSLDKTIKTVWNYITGECISTYRGHSVSLS 387
 Qy 326 LRFESNGLMVTCSDORSIAVDMASATDITLRRVLVGHRAA VNVDFDDKYI--VSASGR 383
 :||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
 Db 388 VDVSQKVIIVSGSADKTVKVHVESRTCVTLR---GHEWVNCVKLHPKSFCSFCSDDT 443
 Qy 384 TIKVWTSTCEFTVTLNGH---KRGIAQLQVRD--RLVVSSG----- 421
 :||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
 Db 444 TIRMWDIRTNSCLKFRGHVGQVKIIPLATIKOVLENLATDNTSGSSPQDDPTMTDGADE 503
 Qy 422 -----DNTIRLWDIECGACRLVLEGHEELVRCIRFDNK 454
 :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
 Db 504 SDTPSNQEVTLVDNIPIYPHTLLSCGLDNTIKJMDVTGKCIRTOFGHVEGWDIAADNF 563
 Qy 455 RIVSGAYDGKIKVMDLAALDPRAPASTLCURTIVEHSGRVRFLQDFEQIISSSHDDTI 514
 :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
 Db 564 RLISGSHDGIKWDLQ-----SGKCNWTF---NGR--RLQRE-----TQHTQTQ 603
 Qy 515 LIWDFLNPPSA 526
 :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
 Db 604 SLGD-KVAPIA 613

RESULT 6
 T46660
 sulfur controller-2 protein [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
 C:Accession: T46660
 R:Kumar, A.; Paietta, J.V.
 Proc. Natl. Acad. Sci. U.S.A. 92, 3343-3347, 1995
 A>Title: The sulfur controller-2 negative regulatory gene of Neurospora crassa
 A:Reference number: 223121; MUID:95241499; PMID:7724564
 A:Accession: T46660
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-650 <RUM>
 A:Cross-references: UNIPROT:Q01277; UNIPARC:UPI000013566D; EMBL:U17251; NID:988
 C:Genetics:
 A:Gene: scon-2
 A:Map position: 3
 A:Introns: 75/3; 319/1; 354/1
 C:Function:
 A>Description: negatively regulates sulfur structural gene expression
 A>Note: scon-2+ expression is dependent on CVS3 function and the binding of CY3

Query Match 18.2%; Score 525; DB 2; Length 650;
 Best Local Similarity 24.2%; Pred. No. 8.7e-32;
 Matches 155; Conservative 93; Mismatches 196; Indels 196; Gaps 16

Qy 38 CLQMPBSVRCLOISNGTSSVIVSKRPSEGNYQKEKDLCKIKYFDQWSQSDDQVFVEH--- 94
 Db 44 CYRHHPDSKRNRAADKAKWMI-----QSE-----LDKLTGADQ-QATHWVS 85

[illegible]

RESULT 7
 S62507
 hypothetical trp-asp repeat-containing protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 05-Oct-2004
 C:Accession: T38502; S62507
 R:Jones, L.; Murphy, L.; McNeill, A.; Simpson, I.; Harris, D.; Barrell, B.G.; Rajandream, A.
 submitted to the EMBL Data Library, October 1995
 A:Reference number: Z21798
 A:Accession: T38502
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-267 <J02>
 A:Cross-references: UNIPARC:UPI0000169029; EMBL:Z66525; NID:gl044926; PIDN:CAA91423.1; F:
 C:Genetics:
 A:Map position: 1
 F:18-51/Domain: WD repeat homology <WD1>
 F:104-137/Domain: WD repeat homology <WD2>

Query Match	17.9%	Score 516.5	DB 2	Length 267
Best Local Similarity	38.7%	Pred. No. 1.le-31		
Matches 106	Conservative 54	Mismatches 85	Indels 29	Gaps 6
Qy	259	DNSIKIWDKTSLECLKVLTKHTGTSVLCLOYDER--VIVTSGSDSTVRVWDVNTGEVLTNTL	316	
Db	1	DRTVSVDVNSRFILYKLYGHSGSVCLDFCRRRLNVVSGSDSTIIWQNRRLPKVY	60	
Qy	317	IHNHEAVLHLPNSGLMWTCSKDSRIAYW--DMASATDITLRRVLVGHRAAVNVVDFDDK	374	
Db	61	FGHTDNLVGVVVSNNYIISSSRDHTARVWLDAITSPAEACM-HVLRGHLASVNSVQYSSK	119	
Qy	375	--YIVASGDRTIKWVSTSTCEFTVTLGHKRGKACLOVRDLVVGSSGSDNTIRLWDIEC	432	

[illegible][illegible]

RESULT 9

T18521
beta transducin-like protein - Podospora anserina
C:Species: Podospora anserina
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18521
R:Saupé, S.; Turcq, B.; Regueret, J.
Gene 162, 135-139, 1995
A:Title: A gene responsible for vegetative incompatibility in the fungus Podospora anserina
A:Reference number: Z18944; MUID:96009891; PMID:7557402
A:Accession: T18521
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1356 <SAU>
A:Cross-references: UNIPROT:Q00808; UNIPARC:UPI000012C621; EMBL:L28125; NID:g607002; PID:218521
C:Genetics:
A:Gene: het-el
A:Introns: 761/3

Query Match		16.3%;	Score 468.5;	DB 2;	Length 1356;
Best Local Similarity		28.7%;	Pred. No. 4.6e-27;		
Matches 144;		Conservative 74;	Mismatches 189;	Indels 95;	Gaps 20;
Qy	76	CIKYPQNSQDQVEFVEHLISRMCH--YQGHIN----	SYLKPMQLORDFTALPEOGL	128	
Db	698	CIYWDHLR-----DLVSTSSKVVHLLQDDGDIHRFLT	TKYLVWLEALSILRALPE-GI	751	
Qy	129	DHI--AENILSVLDARSLCAELVCKEQRVISEGMLWKKLIER	MVRTDPLWKGLSERRG	186	
Db	752	NAIRQLESLLGHTIRGLIA-----IVRDGYRFALS	YRMIEKAPLQAYTS----	797	
Qy	187	WDQYLFKNRPTDGPNSVRSLYPKIIQDIETIESNWR	CGRHNL-----	230	
Db	798	--ALVF--APTDSMIKKIFKKEEPGWISTISVVEA	EWACTQTLEGGSSVLSVAFSADG	853	
Qy	231	QRIQCRSENSK-----GVYCLQY--DDEKII	ISGLRDNISIKIWDKT	268	
Db	854	QRVASGDDTKIKIWDATSGTGTQTLEGGGWSVAFSP	DRERVASGDDTKIKIWDAA	913	
Qy	269	SLECLKVLTGHTGSLVCLQY--DERVITGSSDSTVR	VDVNTGVTILHNEAVLHL	326	
Db	914	SGTCTQTLEGGGRVQSVAFSPDQGRVASGDDHTIKI	WDAAASGTCTQTLEGGSSVLSV	973	
Qy	327	RFS-NGLMVTG-SKDRSTAVWDMASATDITLRRVL	VGHRAAVNVVDF--DDKYIVSASGD	382	
Db	974	AFSPDQGRVASGDDTKIKIWDATSG-----TCTQ	LEGGGWSVAFSPDQGRVASGDD	1030	
Qy	383	RTIKWSTSTCFVTRLNGHKGIAQLQYR--DRLVVG	SSDNTIRLWDIECGACLRVLE	440	
Db	1031	KTIKIWDATSGTCTQTLEGGGWSVQSVFSPDQGR	VASGDDHTIKIWDVSGTCTQTL	1090	
Qy	441	GHEELVRCIRF--DNKRIVSGAYDGKIKVWDLQA	ALDPRAPASTLCRLTVHSGRVFRL	498	
Db	1091	GHGDSVWSVAFSPDQGRVASGIDGTIKIWD-----	AASGTCTQTLEGGGWSVHSV	1141	
Qy	499	QF--DEFQIISSHDDTILWD	518		
Db	1142	AFSPDQGRVASGIDGTIKIWD	1163		

RESULT 10

T45136
WD repeat protein popl [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T45136; T40157
R:Kominami, K.; Toda, T.
submitted to the EMBL Data Library, September 1996
A:Description: Fission yeast WD repeat protein Popl is involved in maintenance of ploidy
A:Reference number: Z22925
A:Accession: T45136
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA

A:Residues: 1-775 <KOM>

A:Cross-references: UNIPROT:p87060; UNIPARC:UPI0000131F34; EMBL:Y08391; PIDN:CAA69671.1
A:Experimental source: strain h- 972
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z21842
A:Accession: T40157
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-775 <WOO>
A:Cross-references: UNIPARC:UPI0000131F34; EMBL:AL022103; PIDN:CAAL7898.1; GSPDB:GN00067
A:Experimental source: strain 972h-; cosmid c2G2
C:Genetics:
A:Gene: SPBC2G2.18
A:Map position: 2
A:Note: popl+

Query Match 15.7%; Score 453; DB 2; Length 775;
Best Local Similarity 26.9%; Pred. No. 3.2e-26;
Matches 135; Conservative 80; Mismatches 207; Indels 80; Gaps 11;

Qy	51	SNGTSSVIVSRKRPSEGNVQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQGHINSY	110		
Db	232	SSENPSTHPSNHLSSQKNVAVLKLAQLISSFKLPESVQYLLFHLSCGRIAVQNIHKI	291		
Qy	111	LKPMQLORDFTALPEOGLDHIHAENILSVLDARSLCAELVCKEQRVISEGMLWKKLIER	170		
Db	292	LLPIFKQNFLLGFPAE-----ITNLVLTHLDAPSLCAVQSVSHHWYKLVSS-----	337		
Qy	171	MVRTDPLWKGLSERRG--WDQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNWR	228		
Db	338	--NEELWKSFLKDGPFWDSDSKIRTMCLEQSLSACAIMKRVYFRHFNRLRERWLHAPE	394		
Qy	229	NLQRIQCRSENSKVYCLQYDDEKIIISGLRDNISIKIWDKTSLECLKVLTGHTGSLVCLQY	288		
Db	395	KIKRCSPFIHGVRLLTKLQFDDDKIIIVSTCSPRINYDTKTGLVIRSLSEHEGDDVTFEY	454		
Qy	289	DERVITGSSDSTVRVDVNTGVTILHNEAVLHRLFSGNLGMLVMTCKDRSIAVWDMA	348		
Db	455	VGDTILVGTSTRTVRVWDLRTGCKQVFGHTSIKIKIVQGNQSTTDD-----	505		
Qy	349	SATDITLRRVLVGHRAAVNVVDFDDKYIVSASGORTIKWS-----	389		
Db	506	--DVEKE-----NRPASNDANSMPPIYISSRDCITRLWSLPLCLDDPPFVNVNENPDQ	557		
Qy	390	-----TSTCFVTRLNGHK--RGIACLOYERDLVVGSSDNTIRLWDIECGACLRVLE	440		
Db	558	NDFTSATNPPIYIRTLRHTSDTSVREVACL---GDLIVSASYDGLTVRWKASTGVC	614		
Qy	441	GHEELVRCIRFDNKR--IVSGAYDGKIKVWDLQAALDPRAPASTLCRLTVHSGRVFRL	498		
Db	615	GHVGRVSVTINPRQOCISAGTDAKIRWNLE-----SGELLQTLHGHSNLVSOV	665		
Qy	499	QFDEFQIISSS--HDDTILWD	518		
Db	666	TFNQNLIVSASAPDPTSLRVWD	687		

RESULT 11

AE1810
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: A51810
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Tanaka, K.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE1810
A:Status: preliminary
A:Molecule type: DNA

A;Residues: 1-1227 <KUR>
A;Cross-references: UNIPROT:Q8Z0R1; UNIPARC:UPI000000CDBE5; GB:BA000019; PIDN:BAB77553.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr0029

Query Match 14.8%; Score 425; DB 2; Length 1227;
Best Local Similarity 25.3%; Pred. No. 7.9e-24; Mismatches 192; Indels 112; Gaps 23;
Matches 139; Conservative 106;

```
Qy 23 WLGCANLVESMCALSCLOSMPFVRCLQISNGTSSVIVSRKRPBEGNYOKE-----KDLG 76
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 401 WLTESPIKWEALESLLRR-----SLIEKASTLIEKASTTGGEKEAESRFGLESVV 454
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 77 IKYFDQWSESDQVEFVHLLSRMCHYQGHINSYLPKMLQDFITALPEQGLDHAENIL 136
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 455 MEVI-----TAKFIENSLEEF-----SQTKKL---DFINTYP----- 483
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 137 SYLDARSLCAELVCKEQRVISSEGLWKKL-----IERMVRTDPLWKLSERRG 186
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 484 -LMKARSL---DYIRQIERLILEPVRQKLLNIFGTLEHLHRLRLGT--LOKEPLPKG 537
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 187 W-----DOYLFKNRPTDGPNSFYRSL-----YPKIQTDTETIESNWRGCRHN 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 538 YAAGNLINLRQLQLDKIPESPIDLSGRDFSGLTIQWAFKEVKLKETIFAN-----SD 592
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 230 LQRIQCRSENSKGYVCLQY--DDEKIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVCLQ 287
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 593 LTG-SVFTETMSSVSVKFSFGDKGYFATGLMNGEIRLWQSDNKLRIYKGTAWWAF 651
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 288 Y--DERVIVTGSSDSTVRVDVNTGEVLNLIHNEAVLHFRS--NGLMVTCKDRSIA 343
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 652 FSPDSRLMASGADSTKLMDVHTGECLTKLSKNTKNKYVSVPDGRILASASQDQTIK 711
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 344 VMDMASATDITLRLVLGHRAANVVDV-----DDK--YIVSASGDRTIKVMSTSTCFVR 397
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 712 LWDIATG---NCQOTLIGHDDWWSVTFSPVTDRLPILLASSADQHLKLDVATGCKLK 768
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 398 TLNGHKRGIAQLQYR--DRLVWSSDNTIRLWDIEGACLRVLEGLVLEHVRIRF--DN 453
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 769 TLKGTREHVSVPSPDQTLASSGEDSTVRLMDVKTGCQWQIPEGHSKKVYSVRFSPDG 828
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 454 KRIVSGAYDGKIKVDLQALDPRAPASTLCRLTLVHSGRVPFLQF--DEFQIISSHD 511
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 829 QTLASCGEDRSIKLMDIQRG-----ECVNTLWGHSSQWAIAPSPDGTLLISGDD 879
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 512 DTILIMDFL 520
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 880 QTARLMDVI 888
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 12
S56245
cell division control protein CDC4 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YFL009w
C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence_revision 12-Apr-1996 #text_change 05-Oct-2004
C;Accession: S56245; S48310; A26867; S62304
R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu
submitted to the EMBL Data Library, May 1995
A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces ce
A;Reference number: S56186
A;Accession: S56245
A;Molecule type: DNA
A;Residues: 1-779 <MUR>
A;Cross-references: UNIPROT:P07834; UNIPARC:UPI0000127254; EMBL:D50617; NID:GB36685; PID
R;Churcher, C.
submitted to the EMBL Data Library, September 1994
A;Reference number: S48310
A;Accession: S48310
A;Molecule type: DNA
A;Residues: 1-579 <CHU>
A;Cross-references: UNIPARC:UPI0000168A6E; EMBL:Z46255; NID:G555925; PIDN:CAA86341.1; PI

R;Vochem, J.; Byers, B.
J. Mol. Biol. 195, 233-245; 1987
A;Title: Structural comparison of the yeast cell division cycle gene CDC4 and a related
A;Reference number: A26867; MUID:88011240; PMID:3309335
A;Accession: A26867
A;Molecule type: DNA
A;Residues: 1-459, 'E', 461-779 <YOC>
A;Cross-references: UNIPARC:UPI0000143E17; EMBL:X05625; NID:G3502; PIDN:CAA29113.1; PID:
R;Murakami, Y.
submitted to the EMBL Data Library, April 1994
A;Reference number: S62302
A;Accession: S62304
A;Molecule type: DNA
A;Residues: 1-779 <WU>
A;Cross-references: UNIPARC:UPI0000127254; EMBL:D31600; NID:G836814; PIDN:BAA06495.1; PI
C;Genetics:
A;Gene: SGD:CDC4
A;Cross-references: SGD:S0001885; MIPS:YFL009w
A;Map position: 6L
A;Function:
C;Description: Initiation of DNA replication; separation of the spindle pole bodies to fr
C;Keywords: cell cycle control
F;459-494/Domain: WD repeat homology <WD1>
F;628-659/Domain: WD repeat homology <WD2>

Query Match 14.5%; Score 418; DB 2; Length 779;
Best Local Similarity 25.5%; Pred. No. 1.4e-23;
Matches 128; Conservative 82; Mismatches 160; Indels 132; Gaps 17;

```
Qy 95 LIIRCHYQHGHSYKPLMLQDFITALPEQGLDHAENILSYLDARSLCAELVCKEW 154
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 LVANMRSELSLGTGLKDKDLITSLPFE----ISLKIPNYLQFEDIINSIGVSNW 305
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 155 QRVISG-MLWKKLIERMVRTDPLWKLSESR----RGWQYLFKNRPTDGPNSFYRSL 209
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 NKIIRKSTSLWKKLL-----ISENFVSPKGFNSLNK-----LSQKY 342
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 210 PKIIOD-----IET--IESNRCGRHNLQICRSENSKGYVCLQYDDEKIIISGLRDN 260
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 343 PKLSQQDRRLSLFLENIFILKNYNPKFPVQRTTLRGHMTSVITCLQFEDNYVITGDDK 402
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 261 SIKIWDKTSLECLKVLGTGHTGSLVCLQYDE-RVIVTGSSDSTVRVMDVNTGEVLNLIHH 319
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 403 MIRVYSINKFLLQSLGHDGWWALYAHGGILVSGSDTRTVRVWDIKKG----- 453
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 320 NEAVLHLRFNSGLMVTCKDRSIAVMDASATDITLRLVLGHRAANVVDVDD-----KY 375
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 454 -----CCT-----HVFKGHNSTVRCLDIVEYKNIKY 479
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 376 IVSASGDRTIKVMST-----STCE-----FVRLNGHKRGIAQLQYR 412
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 480 IVTGSRDNTLHWKLPKESVDPHGEHDYPLVFTHTPEENPYFVGLRGHMASVRTVSGH 539
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 413 DRLVWSSDNTIRLWDIEGACLRVLEGLVLEHVRIRFDPN--KRIVSGAYDGKIKVWDL 470
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 540 GNIVSGSYDNTLIVMDVAQMKCLYLISGHTDIYSTIYDHERKRCISASMDTIRIWDL 599
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 471 Q-----AALDPRAPASTL--CURLTVEHSGRVPFLQFDEFQIISSHDITILWDF 519
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 600 ENIWNNGECSYATNSASPCAKILGAMVTLQHTALVGLRLSKFLVSAADSGIRGWD- 658
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 520 LNVPPPSAQNETRSPRSTYTIIS 541
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 659 -----ANDYSRKFSYHHTNLS 674
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 13
T43557
F-box/WD-repeat protein pop2 - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: proteolysis factor sudlp
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43557; T38794; T43798

R;Wolf, D.A.; Jackson, P.K.
A:Submitted to the EMBL Data Library, December 1997
A:Description: Fission yeast pop2 encodes a novel F-box/WD-repeat protein involved in the
A:Reference number: Z22576
A:Accession: T43557
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-703 <WOL>
A:Cross-references: UNIPROT:O14170; UNIPARC:UPI0000131F36; EMBL:AF038867; PIDN:AAB95480.
A:Experimental source: strain h- 972
R;Gentles, S.; Churcher, C.M.; Barrrell, B.G.; Rajandream, M.A.; Wood, V.
A:Submitted to the EMBL Data Library, August 1996
A:Reference number: Z21812
A:Accession: T38794
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-703 <GEN>
A:Cross-references: UNIPARC:UPI0000131F36; EMBL:Z98602; PIDN:CAB11275.1; GSPDB:GN000066;
A:Experimental source: strain 972h-; cosmid c4D7
R;Jallepalli, P.V.; Tien, D.; Kelly, T.J.
Proc. Natl. Acad. Sci. U.S.A. 95, 8159-8164, 1998
A:Title: Sud1+ targets cyclin-dependent kinase-phosphorylated Cdc18 and Rum1 proteins for
A:Reference number: Z22686; MUID:98318628; PMID:9653157
A:Accession: T43798
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-703 <JAL>
A:Cross-references: UNIPARC:UPI0000131F36; EMBL:AF064515; NID:g3293382; PIDN:AAC39496.1;
A:Experimental source: pop2; sud1; SPAC4D7.03
C:Genetics:
A:Gene: pop2; sud1; SPAC4D7.03
A:Map position: 1
C:Function:
A:Description: required to prevent spontaneous re-replication

Query Match 13.5%; Score 389.5; DB 2; Length 703;
Best Local Similarity 23.3%; Pred. No. 1.8e-21;
Matches 143; Conservative 113; Mismatches 232; Indels 127; Gaps 25;

QY 3 PDSVIEDKTIELMCSVPRLWGLCANLVESMCAL--SCLOSMPSVRCLOISNCTSS-----56
DB 114 PDSVPGDFSISL---VPQ-----RNFLYSHSLPPIKTIISDRNRRIKLDNISNSNDF 164
QY 57 ---VIVSRKRPSEGNVQKEKDL-----CIKYPDQWSESDQVEFVEHLISRMCHYOHG 105
DB 165 PPSPKVDTSNTVSPSKPISEDELDNLQSIQVOTEDIPGQI-QSYAFQQLRSNCNRSQM 223
QY 106 H-INSYLPMLQDFITAPLPEGLDHIHAEINILSYLDARSLCAEALVCKEQRVIS-EGWL 163
DB 224 RLLNECEPLKKOILSNLPFS---IVQSILLNLDIHSFLSCLVSPPTWNRILDVHTSY 279
QY 164 WKLLIE---RMVRTDPLWGLSERRGWDQYLFKRPTDGP-PNSFYRS-----LYPK 211
DB 280 WKHMFSLFGQINEND--WKYANPNLNRPPFLHNDQISDDYEPPEIFKRHFLNRKWLFPFS 337
QY 212 ITQD-----IETIENWRCGRHNLQR---IQCRSENSK-GVYCL 246
DB 338 IPPSHLSPIHPVNFMTISLLHKDRIITTSQSGIIQHNAITGVLEARLEGKEGVAV 397
QY 247 QYDDEKIIISGLRDSIKIWDKTSLECLKVLGTGHTGSLVLCQY-----DE 290
DB 398 KIHENTLVSGSIDKTVRVWNIEKAKCTHIFRGHISIIRCLEILVPSRLIRHGVEIVEPDQ 457
QY 291 RVIVTGSSDSTVRVDV-----NTGBV-----LNTLIHNEAVLHLRFSN 330
DB 458 PYIVSGSRDHLRVWKLPRNTDPPYLPDNTNSIDRWKNPYFVHTLIGHTDSVRTISGVG 517
QY 331 GLMVTCSKDRSAVNDMASATDITLRRVLVGHRAAVNVVDPDK--YIVSASGDRITIKW 388
DB 518 DLLVSGSYDSSIRIRVSTGECYIHLR---GHSIRIYSLVYPERNICISGSMDSKIRW 574
QY 389 ---STCSTCFVRLNGHKGAGIACQYLRDLRVSGSSDNTIRLWDIECGACLRVLEGHEELV 446
DB 575 DLSTGCTCKYV--LEGHDAFVTLNLFVQNRLISSADSTIRIWDLNTGKPLMWLPNSGYI 632

QY 447 RCIRFDNKRIVSGAYDGKIKVMDLOALDPRAPASTLCRLTIVHSGRVFRLOQDFEQII 506
DB 633 SSFVSDHEKIIISG-NDGSKVLMWDVETG-----KLLRFLTLDTLTKIWHVDFDAMRCV 682
QY 507 SSSHDDTILIWDFLN 521
DB 683 AAVQRDDQAYLEVIN 697
RESULT 14
A:12493
WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: A12493
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: A12493
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1189 <KUR>
A:Cross-references: UNIPROT:Q8YL09; UNIPARC:UPI00000CEEDC; GB:BA000020; PIDN:BA078213.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr7129
A:Genome: plasmid

Query Match 13.5%; Score 387.5; DB 2; Length 1189;
Best Local Similarity 28.4%; Pred. No. 5.3e-21;
Matches 91; Conservative 66; Mismatches 112; Indels 51; Gaps 9;

QY 250 DEKIISGLRDSIKIWDKTSLECLKVLGTGHTGSLVLCQYDER--VIVTGSSDSTVRVMDV 307
DB 784 DNLLLSGSDQSVKWDRTKGTGCLDTLAKKHTNRISVAFHPQGHFLFVSGDDHAAKIWEI 843
QY 308 NTGEVLNLIHNEAVLHL--RFSNGLMVTCSKDRSIAVDM-----ASATDITLRRVL 359
DB 844 GTGQCIKTFQGSNATYTIHNEHSLASGHEDQTIKLWDLNLHSPKSNVNTHPFRL 903
QY 360 VGHRAAVNVDFDD--KYIVSASGDRITIKVWSTSCFVRTLNHGRGIACIQLYR--DRL 415
DB 904 QGHSNRFVSFVSTGTQQLASGADRTIKLWSPHTGQCLHTLHGHSWWAIFSLDDKL 963
QY 416 VVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF--DNKRIVSGAYDYGKIKVMDLQ-- 471
DB 964 LASGYDHTVKIWDVSSGQCLQTLQGHPGSVLAVAFSCDGKTLFSSGYEKLVKQWDVETG 1023
QY 472 -----AALDPRAPAS-----TLCLRTLVEHSGRVRFRLOQ 500
DB 1024 YCLOTWEADSNRVAVAVSRDQVNLATGDDSDSVRLWLDIGKVCVTRFSGHTSOVICILF 1083
QY 501 --DEPQIISSHDDTILWID 518
DB 1084 TKDGRRMISSDRTIKIWN 1103

RESULT 15
A:1842
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: A1842
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AC1842
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1747 <KUR>
A;Cross-references: UNIPROT:Q8Z020; UNIPARC:UPI000000CDCC1; GB:BA000019; PIDN:BAB77807.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all0283

Query Match	13.3%	Score 383.5;	DB 2;	Length 1747;
Best Local Similarity	33.5%	Pred. No. 1.8e-20;		
Matches	85;	Conservative	51;	Mismatches 99; Indels 19; Gaps 8;

Qy	229	NLQRIQCRSEKGVYCLQY--DDEKIIISGLRDNISIKWDKTSLECLKVLTHGTGSLVCL	286
Db	1468	SLSTIQ---KNQNIITTVSYSPDGKTIATASADNTIKLWDSQTOQLIKTLTHKDRITTL	1524
Qy	287	QY--DERVIVTGSDDSTVRVMDVNTGEVLAATLIHNEAVLHLRF--NGLMVTCSKDRSI	342
Db	1525	SFHPDNTIASGSADKTIKIWRVNDGQLRLTLTGHNDVTSVNFSPDQQLASGSTDNTV	1584
Qy	343	AVMDMASATDITLRVLVGHRAAVNVYDF--DDKYIVSASGDRTIKVWSTSTCEFVRLN	400
Db	1585	KIWQ----TDGRLIKNTGHCLAIASVKFSPDSHTLASASWDNTIKLWQVTDGKLINLN	1640
Qy	401	GHRKGIAQLQYR--DRLVVGSSDNTIRLWDIEGACLRVLEGHEELVRCIRF--DNKRI	456
Db	1641	GHIDGVTSLSFSPDGEILASGSADNTIKLWLPNATLLKTLGLHGPBKINTLAFSPDGKTL	1700
Qy	457	VSGAYDGKIKVWDL	470
Db	1701	LSGGEDAGVWVWNL	1714

Search completed: August 25, 2006, 07:23:15
Job time : 44 secs

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -I- FUNCTION: Probably recognizes and binds to some phosphorylated
 CC proteins and promotes their ubiquitination and degradation. May
 CC participate in Wnt signaling.
 CC -I- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex.
 CC -I- SUBCELLULAR LOCATION: Cytoplasm (Potential).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=C;
 CC IsoId=Q9UKB1-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=Q9UKB1-2; Sequence=VSP_006765;
 CC Name=B;
 CC IsoId=Q9UKB1-3; Sequence=VSP_006766;
 CC -I- SIMILARITY: Contains 1 F-box domain.
 CC -I- SIMILARITY: Contains 7 WD repeats.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR ENBL; AF176022; AAF04528.1; -; mRNA.
 DR ENBL; AB033279; BAA92329.1; -; mRNA.
 DR ENBL; AB033280; BAA92330.1; -; mRNA.
 DR ENBL; AB033281; BAA92331.1; -; mRNA.
 DR ENBL; AB014596; BAA31671.1; ALT INIT; mRNA.
 DR ENBL; BC026213; AAH26213.1; -; mRNA.
 DR HSP; Q9Y297; IP22.
 DR Ensembl; ENSG00000072803; Homo sapiens.
 DR H-InVDB; HIX0005413; -.
 DR HGNC; HGNC:13607; FBXW11.
 DR MIM; 605651; Gene.
 DR LinkHub; Q9UKB1; -.
 DR GO; GO:0000151; C:ubiquitin ligase complex; NAS.
 DR GO; GO:0005515; F:Protein binding; IPI.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; NAS.
 DR GO; GO:0016567; P:protein ubiquitination; NAS.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS00181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 5.
 DR PROSITE; PS00082; WD_REPEATS_2; 7.
 DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
 DR Alternative splicing; Repeat; Ubl conjugation pathway; WD repeat;
 KW Wnt signaling pathway.
 CHAIN 1 542 F-box/WD-repeat protein 11.
 FT FTID=PRO_0000050981.
 FT DOMAIN 129 167 F-box.
 FT REPEAT 238 275 WD 1.
 FT REPEAT 278 315 WD 2.
 FT REPEAT 318 355 WD 3.
 FT REPEAT 361 398 WD 4.
 FT REPEAT 401 440 WD 5.
 FT REPEAT 442 478 WD 6.
 FT REPEAT 490 527 WD 7.
 FT VARSPLIC 16 49 Missing (in isoform A).
 FT FTID=VSP_006765.
 FT CSVPRSLWLGANLVESMCALSCIQSMPSVRL -> NTSV

FT MEDONEDESPKNTLW (in isoform B).
 FT /FTID=VSP_006766.
 SQ SEQUENCE 542 AA; 62091 MW; 7CD40087EFAA5C8A CRC64;
 Query Match 100.0%; Score 2879; DB 1; Length 542;
 Best Local Similarity 100.0%; Pred. No. 8.3e-205;
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEPDSVIEDKTIELMCSVPRSLWLGANLVESMCALSCIQSMPSVRLQISNGTSSVIVS 60
 DB |||||
 QY 61 RRPSPGNYQKEKDLCKYFDQWSESDQVEFVEHLISRMCHYOHGHINSYVKPMLQDFI 120
 DB |||||
 QY 61 RRPSPGNYQKEKDLCKYFDQWSESDQVEFVEHLISRMCHYOHGHINSYVKPMLQDFI 120
 QY 121 TALPEQGLDHAENILSYLDARSLCAELVCKEWQQRVISEGMLWKKLIERMVMTDPLWKG 180
 DB |||||
 QY 121 TALPEQGLDHAENILSYLDARSLCAELVCKEWQQRVISEGMLWKKLIERMVMTDPLWKG 180
 QY 181 LSERRGWDQVLFKNRPTDGPNSFYRSLYPKIIQDIETIESNWRGCRHNLQRIQCRSENS 240
 DB |||||
 QY 181 LSERRGWDQVLFKNRPTDGPNSFYRSLYPKIIQDIETIESNWRGCRHNLQRIQCRSENS 240
 QY 241 KGVYCLQYDDEKIIISGLRDNISIKWDKTSLECLKVLGTGTSVLCIQYDERVIVTSSDS 300
 DB |||||
 QY 241 KGVYCLQYDDEKIIISGLRDNISIKWDKTSLECLKVLGTGTSVLCIQYDERVIVTSSDS 300
 QY 301 TVRVMDVTGCVLNTLIHNEAVLHFRSNGMLVMTCSKDRSIAVDMASATDITLRRVLV 360
 DB |||||
 QY 301 TVRVMDVTGCVLNTLIHNEAVLHFRSNGMLVMTCSKDRSIAVDMASATDITLRRVLV 360
 QY 361 GHRAAVNVVDFDDKYIVSAGDRTIKVNSTSTCFVRLTNGHKGACIACLOYRDLVVSGS 420
 DB |||||
 QY 361 GHRAAVNVVDFDDKYIVSAGDRTIKVNSTSTCFVRLTNGHKGACIACLOYRDLVVSGS 420
 QY 421 SDNTIRLWDIECGACURVLEHGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPA 480
 DB |||||
 QY 421 SDNTIRLWDIECGACURVLEHGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPA 480
 QY 481 STLCLRTLVEHSGRVERFLQDFEQIISSSHDDTLIWDFLNVPSPAQNETRSPRTVYI 540
 DB |||||
 QY 481 STLCLRTLVEHSGRVERFLQDFEQIISSSHDDTLIWDFLNVPSPAQNETRSPRTVYI 540
 QY 541 SR 542
 DB ||
 DB 541 SR 542
 RESULT 2
 Q5SRV7_MOUSE PRELIMINARY; PRT; 542 AA.
 ID Q5SRV7_MOUSE AC Q5SRV7;
 DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
 DT 21-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE F-box and WD-40 domain protein 1B (2 days neonate sympathetic ganglion
 DE cDNA, RIKEN full-length enriched library, clone:7120487019 product:F-
 DE box and WD-40 domain protein 1B, full insert sequence).
 GN Names=Fbxw1b; ORFNames=RP23-94F11.1-002;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hopkins B.; (FEB-2005) to the EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Phillimore B.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 [4]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC PubMed=16141072; DOI=10.1126/science.1112014;
 RX Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalis V., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano A., Butler B.D., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G., Fletcher C.F., Fukehima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakaochi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Suglura K., Sultana R., Takenaka Y., Taki K., Tannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamani H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fuda J., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 [5]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC PubMed=16141073; DOI=10.1126/science.1112009;
 RX RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 [6]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC MEDLINE=22354683; PubMed=12466951; DOI=10.1038/nature01266;
 RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragoti T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada M., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Yanagisawa M., Yang L., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [7]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Offelli D., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Bokfield T., Bojunga N., Carninci P., de Bernaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S., Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [8]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RC MEDLINE=20499374; PubMed=1042159; DOI=10.1101/gr.145100;
 RX Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M., Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [10]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
 RX Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,

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RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AL669951; CAI26097.1; -; Genomic DNA.
DR EMBL; AL669844; CAI26097.1; JOINED; Genomic DNA.
DR EMBL; AL669844; CAI25520.1; -; Genomic DNA.
DR EMBL; AL669951; CAI25520.1; JOINED; Genomic DNA.
DR EMBL; AK149139; BAE28749.1; -; mRNA.
DR Ensemble; ENSMUSG0000020271; Mus musculus.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GROTEINERPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS00082; WD_REPEATS_2; 7.
DR PROSITE; PS00082; WD_REPEATS_REGION; 1.
KW Repeat; Ub1 conjugation pathway; WD repeat.
SQ SEQUENCE 542 AA; 62063 MW; D95A78A6977B828A CRC64;

Query Match 99.8%; Score 2872; DB 2; Length 542;
Best Local Similarity 99.6%; Pred. No. 2.8e-204;
Matches 540; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPDSVIEDKTIELMCSVPRSLWLGANLVESMCALSCLOSMPSVRCQLISNGTSVIVS 60
Db 1 MEPDSVIEDKTIELMCSVPRSLWLGANLVESMCALSCLOSMPSVRCQLISNGTSVIVS 60
Qy 61 RKRPSGNYQKEDLCIKYFDQWSESDQVFVEHLISRMCHYOHGHINSYLKPMQLQDFI 120
Db 61 RKRPSGNYQKEDLCIKYFDQWSESDQVFVEHLISRMCHYOHGHINSYLKPMQLQDFI 120
Qy 121 TALPEGLDTHAENILSYLDARSICAELCKEQRVISEGMLWKLIERMVRTDPLWKG 180
Db 121 TALPEGLDTHAENILSYLDARSICAELCKEQRVISEGMLWKLIERMVRTDPLWKG 180
Qy 181 LSERRGWDQVLFKNRPTDGPNSFYRSLYPKIIQDIETIESNRCGRHNLQRIQCRSENS 240
Db 181 LSERRGWDQVLFKNRPTDGPNSFYRSLYPKIIQDIETIESNRCGRHNLQRIQCRSENS 240
Qy 241 KGVYCLQYDDEKIISGLRDSIKIWDKTSLECLKVLGTGHTGSLVCLQYDERVIVTGSDDS 300
Db 241 KGVYCLQYDDEKIISGLRDSIKIWDKTSLECLKVLGTGHTGSLVCLQYDERVIVTGSDDS 300
Qy 301 TVRVWDVNTGEVLNLTLIHNEAVLHFRSGLMVTCSKDRSIAVWDMASATDITLRLVLY 360
Db 301 TVRVWDVNTGEVLNLTLIHNEAVLHFRSGLMVTCSKDRSIAVWDMASATDITLRLVLY 360
Qy 361 GHRAAVNVVDFDDKXIYVSASGDRTIKVMSTSTCEFTVTLNGHKGKGIACQYRDLRVVSGS 420
Db 361 GHRAAVNVVDFDDKXIYVSASGDRTIKVMSTSTCEFTVTLNGHKGKGIACQYRDLRVVSGS 420
Qy 421 SDNTIRLWDIECGACLRVLEGHEBLVRCIRFDNKRIVSGAYDVGKIKWDLOALDPPAPA 480
Db 421 SDNTIRLWDIECGACLRVLEGHEBLVRCIRFDNKRIVSGAYDVGKIKWDLOALDPPAPA 480
Qy 481 STLCLRLTLVHSGRVRLQDFEFOI ISSSHDDTLIWDLFNPPSAQNETRSPRTTYII 540
Db 481 STLCLRLTLVHSGRVRLQDFEFOI ISSSHDDTLIWDLFNPPSAQNETRSPRTTYII 540

541 SR 542
541 SR 542

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RESULT 3
Q8K022 MOUSE
ID Q8K022_MOUSE PRELIMINARY; PRT; 563 AA.
AC Q8K022;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE F-box and WD-40 domain protein 11.
GN Name=Fbxw11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Krangel T.E.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC034261; AAH34261.1; -; mRNA.
DR HSSP; Q9Y297; 1P22.
DR Ensemble; ENSMUSG0000020271; Mus musculus.
DR MGI; MGI:2144023; Fbxw11.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GROTEINERPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS00082; WD_REPEATS_2; 7.
DR PROSITE; PS00082; WD_REPEATS_REGION; 1.
KW Repeat; Ub1 conjugation pathway; WD repeat.
SQ SEQUENCE 563 AA; 64481 MW; 74D07E6B8B50ABED CRC64;

Query Match 99.0%; Score 2851.5; DB 2; Length 563;
Best Local Similarity 95.9%; Pred. No. 9.6e-203;
Matches 540; Conservative 2; Mismatches 0; Indels 21; Gaps 1;

Qy 1 MEPDSVIEDKTIELMCSVPRSLWLGANLVESMCALSCLOSMPSVRCQLISNGTSVIVS 48

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Db 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCQLQNTSVMEQDQNE 60
Qy 49 -----QISNGTSSVIVSRKRPSEGNQYQKEDLCIKYFDQWSESQDQVEFVEHLISRM 99
Db 61 ESPKKSALWQISNGTSSVIVSRKRPSEGNQYQKEDLCIKYFDQWSESQDQVEFVEHLISRM 120
Qy 100 CHYQGHINSYLYKPMQLQDFITALPEQGLDHIENILSYLDARSILCAELVCKEWQVVIS 159
Db 121 CHYQGHINSYLYKPMQLQDFITALPEQGLDHIENILSYLDARSILCAELVCKEWQVVIS 180
Qy 160 EGMWLKLIERMVTRDPLWGLSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETI 219
Db 181 EGMWLKLIERMVTRDPLWGLSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETI 240
Qy 220 ESNWRCGRHNLQIOCRSENSGVYCLQYDDKIIISGLRDNSIKIWDKTSLECLKVLGTH 279
Db 241 ESNWRCGRHNLQIOCRSENSGVYCLQYDDKIIISGLRDNSIKIWDKTSLECLKVLGTH 300
Qy 280 TGSVLCLOYDERVIVTGSSDSTVRVMDVNTGEVLTLLIHNEAVLHLRFSNGLMVTCSKD 339
Db 301 TGSVLCLOYDERVIVTGSSDSTVRVMDVNTGEVLTLLIHNEAVLHLRFSNGLMVTCSKD 360
Qy 340 RSIADVMDASATDITLRLVVGHRAAVNVDFDKKIIVSASGDRTIKVMSTSTCEFVRTL 399
Db 361 RSIADVMDASATDITLRLVVGHRAAVNVDFDKKIIVSASGDRTIKVMSTSTCEFVRTL 420
Qy 400 NGHKGIAQLOYRDLRVVSGSSDNTIRLWDIECGACLRVLEGHVELVRCIRFDNKRIVSG 459
Db 421 NGHKGIAQLOYRDLRVVSGSSDNTIRLWDIECGACLRVLEGHVELVRCIRFDNKRIVSG 480
Qy 460 AYDGKIKVMDLQAALDPRAPASTLCRLTVLHSGRVRFLQDFEQIISSSHDDTLLIWD 519
Db 481 AYDGKIKVMDLQAALDPRAPASTLCRLTVLHSGRVRFLQDFEQIISSSHDDTLLIWD 540
Qy 520 LNVPESAQNETRSPRTTYISR 542
Db 541 LNVPESAQNETRSPRTTYISR 563

RESULT 4
Q923H0 MOUSE PRELIMINARY; PRT; 563 AA.
AC Q923H0;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE F-box/WD40 repeat-containing protein HOS.
GN Name=Fbxw1; Synonyms=Fbxw1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RX MEDLINE=21906231; PubMed=11896578; DOI=10.1038/sj.onc.1205311;
RA Bhatia N., Herter J.R., Slaga T.J., Fuchs S.Y., Spiegelman V.S.;
RT "Mouse homologue of HOS (mHOS) is overexpressed in skin tumors and
RL implicated in constitutive activation of NF-kappaB";
RL Oncogene 21:1501-1509(2002).
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CC -----
CC EMBL: AV038079; AAK72095.1; -; mRNA.
DR HSSP; Q9Y297; 1P22.
DR Ensembl; ENSMUSG00000020271; Mus musculus.
DR MGI; MGI:2144023; Fbxw1b.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
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DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS0181; FBOX; 1.
DR PROSITE; PS00678; WD REPEATS 1; 5.
DR PROSITE; PS0082; WD REPEATS 2; 7.
DR PROSITE; PS0294; WD REPEATS REGION; 1.
KW Repeat; Ubl conjugation pathway; WD repeat.
SQ SEQUENCE 563 AA; 64742 MW; 9AB562F3FF5E3496 CRC64;

Query Match 95.7%; Score 2755.5; DB 2; Length 563;
Best Local Similarity 93.3%; Pred. No. 1.3e-195;
Matches 525; Conservative 2; Mismatches 15; Indels 21; Gaps 1;

Qy 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCQLQNTSVMEQDQNE 48
Db 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPSVRCQLQNTSVMEQDQNE 60
Qy 49 -----QISNGTSSVIVSRKRPSEGNQYQKEDLCIKYFDQWSESQDQVEFVEHLISRM 99
Db 61 ESPKKSALWQISNGTSSVIVSRKRPSEGNQYQKEDLCIKYFDQWSESQDQVEFVEHLISRM 120
Qy 100 CHYQGHINSYLYKPMQLQDFITALPEQGLDHIENILSYLDARSILCAELVCKEWQVVIS 159
Db 121 CHYQGHINSYLYKPMQLQDFITALPEQGLDHIENILSYLDARSILCAELVCKEWQVVIS 180
Qy 160 EGMWLKLIERMVTRDPLWGLSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETI 219
Db 181 EGMWLKLIERMVTRDPLWGLSERRGWDQYLFKNRPTDGPNSFYRSLYPKIIQDIETI 240
Qy 220 ESNWRCGRHNLQIOCRSENSGVYCLQYDDKIIISGLRDNSIKIWDKTSLECLKVLGTH 279
Db 241 ESNWRCGRHNLQIOCRSENSGVYCLQYDDKIIISGLRDNSIKIWDKTSLECLKVLGTH 300
Qy 280 TGSVLCLOYDERVIVTGSSDSTVRVMDVNTGEVLTLLIHNEAVLHLRFSNGLMVTCSKD 339
Db 301 TGSVLCLOYDERVIVTGSSDSTVRVMDVNTGEVLTLLIHNEAVLHLRFSNGLMVTCSKD 360
Qy 340 RSIADVMDASATDITLRLVVGHRAAVNVDFDKKIIVSASGDRTIKVMSTSTCEFVRTL 399
Db 361 RSIADVMDAFCHRYHFTPCSGMPRAAVNVDFDKKIIVSASGDRTIKVMSTSTCEFVRTL 420
Qy 400 NGHKGIAQLOYRDLRVVSGSSDNTIRLWDIECGACLRVLEGHVELVRCIRFDNKRIVSG 459
Db 421 NGHKGIAQLOYRDLRVVSGSSDNTIRLWDIECGACLRVLEGHVELVRCIRFDNKRIVSG 480
Qy 460 AYDGKIKVMDLQAALDPRAPASTLCRLTVLHSGRVRFLQDFEQIISSSHDDTLLIWD 519
Db 481 AYDGKIKVMDLQAALDPRAPASTLCRLTVLHSGRVRFLQDFEQIISSSHDDTLLIWD 540
Qy 520 LNVPESAQNETRSPRTTYISR 542
Db 541 LNVPESAQNETRSPRTTYISR 563

RESULT 5
Q8BY90 MOUSE PRELIMINARY; PRT; 529 AA.
AC Q8BY90;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE 3 days neonate thymus cDNA, RIKEN full-length enriched library,
DE clone:A630019L11 product:F-box/WD-REPEAT PROTEIN 1B (F-BOX AND WD-
DE REPEATS PROTEIN BETA-TRCP2) homolog (F-box and WD-40 domain protein
DE 1B) (Bone marrow macrophage cDNA, RIKEN full-length enriched library,
DE clone:I830054B11 product:F-box and WD-40 domain protein 1B, full
DE insert sequence).
DE Name=Fbxw1b; Synonyms=Fbxw1; ORFNames=RP23-94F11.1-001;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 RX MEDLINE=99279233; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RT Carninci P., Hayashizaki Y.;
 RL "High-efficiency full-length cDNA cloning.";
 RN Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.B., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Humaneck I., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.P., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J.C., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sadelain A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Ono Y., Suzuki H., Kawaji J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense transcription in the mammalian transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikafo I., Osato N., Saito K., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldairelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gisi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelain A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawaji J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
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 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
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 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Bone marrow, and Thymus; STRAIN=C57BL/6J;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Iehli Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE.
RA Phillimore B.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE.
RA Hopkins B.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [11]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-C57BL/6J; TISSUE-Bone marrow;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AK041532; BAC30975.1; -; mRNA.
DR EMBL; AL669844; CAI25519.1; -; Genomic_DNA.
DR EMBL; AL669951; CAI25519.1; JOINED; Genomic_DNA.
DR EMBL; AL669951; CAI26098.1; -; Genomic_DNA.
DR EMBL; AL669844; CAI26098.1; JOINED; Genomic_DNA.
DR EMBL; AK152181; BAE31012.1; -; mRNA.
DR HSPF; Q9Y297; IP22.
DR Ensembl; ENSMUSG00000020271; Mus musculus.
Query Match 92.6%; Score 2665.5; DB 2; Length 529;
Best Local Similarity 92.4%; Pred. No. 5.6e-189;
Matches 512; Conservative 4; Mismatches 1; Indels 37; Gaps 4;
Qy 1 MEPDSVIEDKTIELM-CSV-----PR--SLWLGCANLVESMCALSCLOMPSVRL 48
Db 1 MEPDSVIEDKTIELMNTSVMEDQNEDESPKKSALW----- 35
Qy 49 QISNCTSSVIVSRKPSGNYQKEDLCIKYFDQWSESDQVEFVHLLSRMCHYOHGHIN 108
Db 36 QISNCTSSVIVSRKPSGNYQKEDLCIKYFDQWSESDQVEFVHLLSRMCHYOHGHIN 95
Qy 109 SYLKPMQLQDFITALPEQGLDHIAENILSYLDARSALCAELCKEQRVISEGMLWKLI 168
Db 96 SYLKPMQLQDFITALPEQGLDHIAENILSYLDARSALCAELCKEQRVISEGMLWKLI 155
Qy 169 ERWVTDPLWKLSSRRGWDQYLFKNRPTDGPNSFYRSLYPKTIQDIETIESNRCGRH 228
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Qy 289 DERVIVTSSDSTVRVWDVNTGEVLTNTLIHNEAVLHFRFNSGLMVTCKDORSIAVWDM 348
Db 276 DERVIVTSSDSTVRVWDVNTGEVLTNTLIHNEAVLHFRFNSGLMVTCKDORSIAVWDM 335
Qy 349 SATDITLRRVLVGHRAAVNVVDFDDKIVSASGDRITIKWSTSTCEFTVTLNGHKGRIAC 408
Db 336 SATDITLRRVLVGHRAAVNVVDFDDKIVSASGDRITIKWSTSTCEFTVTLNGHKGRIAC 395

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Qy 529 ETRSPSRITYTISR 542
Db 516 ETRSPSRITYTISR 529

RESULT 6
Q3TLZ8_MOUSE
ID Q3TLZ8_MOUSE PRELIMINARY; PRT; 529 AA.
AC Q3TLZ8;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
DE library, clone:G830018H24 product:F-box and WD-40 domain protein 1B,
DE full insert sequence.
GN Name=Fbxw1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic M.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Anweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalia E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Humnick L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
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RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Silva D., Sinclair B.,
RA Shibata Y., Shimada H., Sugiyara K., Sultana R., Takenaka Y., Taki K.,
RA Tannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grammond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wilmstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,

QY 229 NLQIQCRSENSKGYVCLQYDDDKIISGLRDNISIKIWDKTSLECLKVLTHGHTGSLVCLQY 288
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 DB 276 DERIVITGSSDSTVRVWDVNTGEVLNTLIHNEAVLHLRFSNGLMVTCSKORSIAVWDMA 335
 QY 349 SATDITLRLVLRVGHRAAVNVVDFDDKYIVSASGDRITIKWSTSTCEFTVRTLNGHKGRIAC 408
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 QY 409 LOYDRVLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFNDKRVISGAYDGKIKVW 468
 DB 396 LOYDRVLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFNDKRVISGAYDGKIKVW 455
 QY 469 DLOAALDPRAPASTLCRLTLVHSGRVRFLQDFEFOIISSSHDDTILILWDFLNVPSSAQN 528
 DB 456 DLOAALDPRAPASTLCRLTLVHSGRVRFLQDFEFOIISSSHDDTILILWDFLNVPSSAQN 515
 QY 529 ETRSPSRITYTISR 542
 DB 516 ETRSPSRITYTISR 529
 RESULT 7
 Q3TCGM9_MOUSE
 ID Q3TCGM9_MOUSE *PRELIMINARY; PRT; 508 AA.
 AC Q3TCGM9;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE 17 days embryo kidney cDNA. RIKEN full-length enriched library.
 DE clone:1920043C06 product:F-box and WD-40 domain protein 1B, full
 DE insert sequence (Osteoclast-like cell cDNA, RIKEN full-length enriched
 DE library, clone:1420048G02 product:F-box and WD-40 domain protein 1B,
 DE full insert sequence).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
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 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Imbriato A.,
 RA Ambesi-Imbriato A., Appeller R., Acurallya R.N., Bailey T.L.,
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 RA Hill D., Humnietek L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
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 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
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 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=22346683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Suitana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda I.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21085660; PubMed=1217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,


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DR HSP: Q9Y297; 1P22.
DR Ensembl: ENSMUSG00000020271; Mus musculus.
DR MGI: 2144023; Fbxw11.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINBRPT.
DR ProDom: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS00181; FBOX; 1.
DR PROSITE: PS00678; WD REPEATS_1; 5.
DR PROSITE: PS00082; WD REPEATS_2; 7.
DR PROSITE: PS500294; WD_REPEATS_REGION; 1.
KW WD repeat.
FT NON TER 1
SQ SEQUENCE 555 AA; 63288 MW; 6025496DBAC6A489 CRC64;

Query Match 92.4%; Score 2660; DB 2; Length 555;
Best Local Similarity 93.4%; Pred. No. 1.5e-188;
Matches 506; Conservative 2; Mismatches 0; Indels 34; Gaps 1;

QY 1 MEPDSVIEDKTIELMSCVPSRLWLGANLVESMCALCQSMPSVRCIQISNGTSSVIVS 60
DB 48 MEPDSVIEDKTIELM-----ISNGTSSVIVS 73

QY 61 RKRPSSEGNVQKEDLCIKYFDQWSSDQVEFVEHLISRMCHYQHGHINSYLPMLQRFI 120
DB 74 RKRPSSEGNVQKEDLCIKYFDQWSSDQVEFVEHLISRMCHYQHGHINSYLPMLQRFI 133

QY 121 TALPQGLDHAENILSYLDARSLCAELVCKEWQVISEGMLWKKLIERMVVRTDPLWKG 180
DB 134 TALPQGLDHAENILSYLDARSLCAELVCKEWQVISEGMLWKKLIERMVVRTDPLWKG 193

QY 181 LSEREGWQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNRCGRHNLQIQRSSENS 240
DB 194 LSEREGWQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNRCGRHNLQIQRSSENS 253

QY 241 KGVYCLQYDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVCLQYDERVIVTGSSDS 300
DB 254 KGVYCLQYDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVCLQYDERVIVTGSSDS 313

QY 301 TVRVWDVNTGEVNTLIHNEAVLHFRFNSGLMVTCSKDRSTAVWDMASATDITLRRVLV 360
DB 314 TVRVWDVNTGEVNTLIHNEAVLHFRFNSGLMVTCSKDRSTAVWDMASATDITLRRVLV 373

QY 361 GHRAAVNVVDFDKYIVSASGDRTIKVMSTSTCEVFRTILNGHKGRIACIQYRDRLVWSGS 420
DB 374 GHRAAVNVVDFDKYIVSASGDRTIKVMSTSTCEVFRTILNGHKGRIACIQYRDRLVWSGS 433

QY 421 SNTIRLWDIEGACLRVLEGEHELVRICIRFONKRIVSGAYDGKIKVWDLQAALDPRAPA 480
DB 434 SNTIRLWDIEGACLRVLEGEHELVRICIRFONKRIVSGAYDGKIKVWDLQAALDPRAPA 493

QY 481 STLCLRTLVHSGRVRFLQDFEQIISSSHDDTILWDFLNPVPPSAQNETSPSRITYI 540
DB 494 STLCLRTLVHSGRVRFLQDFEQIISSSHDDTILWDFLNPVPPSAQNETSPSRITYI 553

QY 541 SR 542
DB 554 SR 555

RESULT 9
Q5ZH09 CHICK
ID Q5ZH09_CHICK PRELIMINARY; PRT; 529 AA.
AC Q5ZH09;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Hypothetical protein.
GN ORFNames=RCJMB04_34f17;

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCHI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatki A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis.";
RL Genome Biol. 6:R6-R6(2005).
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CC -----
DR EMBL: AJ721075; CAG32734.1; -; mRNA.
DR GO: GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINBRPT.
DR ProDom: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PS00181; FBOX; 1.
DR PROSITE: PS00678; WD REPEATS_1; 5.
DR PROSITE: PS00082; WD REPEATS_2; 7.
DR PROSITE: PS500294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; Ub conjugation pathway; WD repeat.
SQ SEQUENCE 529 AA; 60924 MW; 0DCD9905P5D0F1E7 CRC64;

Query Match 92.1%; Score 2652.5; DB 2; Length 529;
Best Local Similarity 91.9%; Pred. No. 5.1e-188;
Matches 509; Conservative 2; Mismatches 6; Indels 37; Gaps 3;

QY 1 MEPDSVIEDKTIELM-CSV-----PRLWLGANLVESMCALCQSMPSVRCIL 48
DB 1 MEPDSVIEDKTIELMNTSVMEDQNEDESPKNTLM----- 35

QY 49 QISNGTSSVIVSRKRPSEGNVQKEDLCIKYFDQWSSDQVEFVEHLISRMCHYQHGHIN 108
DB 36 QISNGTSSVIVSRKRPSEGNVQKEDLCIKYFDQWSSDQVEFVEHLISRMCHYQHGHIN 95

QY 109 SYLKPMLQRFITLPEQGLDHAENILSYLDARSLCAELVCKEWQVISEGMLWKKLI 168
DB 96 SYLKPMLQRFITLPEQGLDHAENILSYLDARSLCAELVCKEWQVISEGMLWKKLI 155

QY 169 ERMVVRTDPLWKLSERRGWQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNRCGRH 228
DB 156 ERMVVRTDPLWKLSERRGWQYLFKNRPTDGPNSFYRSLYPKIIQDIETIESNRCGRH 215

QY 229 NLRIQCRSENSKGVYCLQYDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVCLQY 288
DB 216 NLRIQCRSENSKGVYCLQYDDEKIIISGLRDNISIKIWDKTSLECLKVLGTGHTGSLVCLQY 275

QY 289 DERVIVTGSSDSTVRVWDVNTGEVNTLIHNEAVLHFRFNSGLMVTCSKDRSIWDMNA 348
DB 276 DERVIVTGSSDSTVRVWDVNTGEVNTLIHNEAVLHFRFNSGLMVTCSKDRSIWDMNA 335

QY 349 SATDITLRRVLVGHRAAVNVVDFDKYIVSASGDRTIKVMSTSTCEVFRTILNGHKGRIAC 408
DB 336 SPTDITLRRVLVGHRAAVNVVDFDKYIVSASGDRTIKVMSTSTCEVFRTILNGHKGRIAC 395

QY 409 LOYRDLRVVSGSSDNTIRLWDIEGACLRVLEGEHELVRICIRFONKRIVSGAYDGKIKVW 468
DB 396 LOYRDLRVVSGSSDNTIRLWDIEGACLRVLEGEHELVRICIRFONKRIVSGAYDGKIKVW 455

QY 469 DIQAALDPRAPASTLCLRTLVHSGRVRFLQDFEQIISSSHDDTILWDFLNPVPPSAQ 528
DB 469 DIQAALDPRAPASTLCLRTLVHSGRVRFLQDFEQIISSSHDDTILWDFLNPVPPSAQ 528

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Db 456 DLQALDPRAPASTLCRLTLVHSGRVRFLQDFEQIISSSHDDTLIWDFLNVPSPAPN 515
Qy 529 ETRSPRTTYISR 542
Db 516 ETRSPRTTYISR 529

RESULT 10
Q6PGW4 BRARE
ID Q6PGW4 BRARE PRELIMINARY; PRT; 527 AA.
AC Q6PGW4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 17.
DE zgc:63728.
GN ORFNames=zgc:63728;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whaley J., Helton E., Kettelman M., Madan A., Rodriguezes S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.F.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; BC056809; AAH56809.1; -; mRNA.
DR Ensembl; ENSDARG0000017230; Danio rerio.
DR ZFIN; ZDB-GENE-040426-2903; zgc:63728.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR PRODOM; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS00082; WD_REPEATS_2; 7.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; Ub1 conjugation pathway; WD repeat.
SQ SEQUENCE 527 AA; 60547 MW; 563F3C014CA099C3 CRC64;
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Best Local Similarity 86.1%; Pred. No. 7e-173;
Matches 466; Conservative 30; Mismatches 26; Indels 19; Gaps 4;

Qy 7 IEDKTIELMCSVPRSLWGLCANLVESMCA-----LSCLQSMPSVRCLQISNGTSSVIVSR 61
Db 1 MEDKTIELQNT-----SVMDPQTADRSKPTLIKSS--TFICPQVSNQ--PLTGSR 46

Qy 62 KRPSGNYOKEKDLCTKYFDQWSESQVFEVHILSRMCHYQHGHINSYLNKPLQDRDFIT 121
Db 47 KRPSGNYEKEKDVCTQLFDQWSEADQVFEVHILSRMCHYQHGHINSYLNKPLQDRDFIT 106

Qy 122 ALPEQGLDHAENILSYLDARSLCAAEVLCKEQRVISEGMLWKKLIERVTRDPLWKGL 181
Db 107 ALPAQGLDHAENILSYLDARSLCAAEVLCKEQRVISEGMLWKKLIERVTRDPLWKGL 166

Qy 182 SERRGMDQVLFKNRPTDGPNSFYRLPKIIQDIETIESNMWRCGRHNLQRIQCRSENSK 241
Db 167 SERHQWEKYLFKORTTEVPNSYRSLPKIIQDIETIEANWRCGRHNLQRIQCRSENSK 226

Qy 242 GVCLOYDDEKIIISGLRDSIKIWDKYSLECLKVLTGHTGSLVCLQYDERVIVTGSSDST 301
Db 227 GVCLOYDDEKIIISGLRDSIKIWDKQTLKLTGHTGSLVCLQYDERVIVTGSSDST 286

Qy 302 VRVMDVNTGEVLNLTLIHNEAVLHLFNSGLMVTCSKDRSIAVMDMASATDITLRRVLVG 361
Db 287 VRVMDVNSGEVLNLTLIHNEAVLHLFNSGLMVTCSKDRSIAVMDMASATDITLRRVLVG 346

Qy 362 HRAAVNVVDFDDKYIVSASGDRTIKWSTSTCEVFRTLNGHKGIAQLQYRDLRVVSGSS 421
Db 347 HRAAVNVVDFDDKYIVSASGDRTIKWSTSTCEVFRTLNGHKGIAQLQYRDLRVVSGSS 406

Qy 422 DNTIRLWDEICGACLRVLSGHEBELVCIRPDNKRIVSGAYDGIKIKWDLQALDPRAPAS 481
Db 407 DNTIRLWDEICGACLRVLSGHEBELVCIRPDNKRIVSGAYDGIKIKWDLQALDPRAPAS 466

Qy 482 TILCLRTLVEHSGRVRFLQDFEQIISSSHDDTLIWDFLNVPSPAQNETSPSRRTYIS 541
Db 467 TILCLRTLVEHSGRVRFLQDFEQIISSSHDDTLIWDFLNVPSPAQNETSPSRRTYIS 526

Qy 542 R 542
Db 527 R 527

RESULT 11
FBW1A HUMAN
ID FBW1A HUMAN STANDARD; PRT; 605 AA.
AC Q9Y297; Q9Y213;
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 52.
DE F-box/WD-repeat protein 1A (F-box and WD-repeats protein beta-TrCP)
DE (E3RS1kappa) (pikappaalpha-E3 receptor subunit).
GN Name=BTRC; Synonyms=BTCP, FBW1A, FBXW1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RX MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;
RA Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
RA Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
RT "Identification of the receptor component of the IkappaBalpha-
RT ubiquitin ligase";
RL Nature 396:590-594 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
RX MEDLINE=98325370; PubMed=9660940; DOI=10.1016/S1097-2765(00)80056-8;
RA Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
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December 10

Thomas D., Strebel K., Benarous R.;
 "A novel human WD protein, h-beta TrCP, that interacts with HIV-1 Vpu connects CD4 to the ER degradation pathway through an F-box motif."; Mol. Cell 1:565-574 (1998).
 [3]
 NP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
 RP MEDLINE=2003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;
 RX Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M., Pagano M.;
 "Identification of a family of human F-box proteins."; Curr. Biol. 9:1177-1179 (1999).
 [4]
 NP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RP TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullenbach S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Wortley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [5]
 NP CHARACTERIZATION.
 RX MEDLINE=99145464; PubMed=9990852;
 RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J., Harper J.W.;
 "The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically with phosphorylated destruction motifs in I-kappa-B-alpha and beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro."; Genes Dev. 13:270-283 (1999).
 [6]
 NP INTERACTION WITH UBQLN1.
 RP TISSUE=B-cell;
 RX MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X;
 RA Kleijnen M.F., Shih A.H., Zhou P., Kumar S., Soccio R.E., Kederha N.L., Gill G., Howley P.M.;
 "The hPLIC proteins may provide a link between the ubiquitination machinery and the proteasome."; Mol. Cell 6:409-419 (2000).
 [7]
 NP INTERACTION WITH PHOSPHORYLATED CTNNB1.
 RX MEDLINE=22072105; PubMed=12077367;
 RA Sadot E., Conacci-Sorelli M., Zhurinsky J., Shnizer D., Lando Z., Zharhary D., Kam Z., Ben-Ze'ev A., Geiger B.;
 "Regulation of S33/S37 phosphorylated beta-catenin in normal and transformed cells."; J. Cell Sci. 115:2771-2780 (2002).
 [8]
 NP X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1 AND CTNNB1.
 RX MEDLINE=22706071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X;
 RA Wu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W., Pavletich N.P.;
 "Structure of a beta-TrCP1-Skp1-beta-catenin complex: destruction motif binding and lysine specificity of the SCF(beta-TrCP1) ubiquitin ligase."; Mol. Cell 11:1445-1456 (2003).
 CC FUNCTION: Substrate-recognition component of the SCF (SKP1-CUL1-F-box protein) ubiquitin ligase complex, which mediates the

ubiquitination of proteins involved in cell cycle progression, signal transduction and transcription. Regulates the stability of CTNNB1 and participates in Wnt signaling.
 CC PATHWAY: Ubiquitin conjugation; third step.
 CC SUBUNIT: Interacts directly with SKP1 in the SCF complex.
 CC Interacts specifically with phosphorylated CTNNB1 and NFKBIA, ubiquitination substrates. Binds UBQLN1.
 CC SUBCELLULAR LOCATION: Cytoplasm.
 CC ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9Y297-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9Y297-2; Sequence=VSP_006764;
 CC SIMILARITY: Contains 1 F-box domain.
 CC SIMILARITY: Contains 7 WD repeats.
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 EMBL: AF101784; AAD08702.1; -; mRNA.
 DR EMBL: Y14153; CAA74572.1; -; mRNA.
 DR EMBL: AF129530; AAF04464.1; -; mRNA.
 DR EMBL: BC027994; AAZ27994.1; -; mRNA.
 DR PDB: 1P22; X-ray; A=175-605.
 DR IntAct; Q9Y297;
 DR Ensembl; ENSG00000166167; Homo sapiens.
 DR HGNC; HGNC:1144; BTRC.
 DR MIM; 603482; gene.
 DR LinkHub; Q9Y297;
 DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS0181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 6.
 DR PROSITE; PS0082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW 3D-structure; Alternative splicing; Ligase; Polymorphism; Repeat;
 KW Ub1 conjugation pathway; WD repeat; Wnt signaling pathway.
 FT F-box/WD-repeat protein 1A.
 FT FTId=PRO_0000050980.
 CHAIN 1 605
 DOMAIN 190 228
 REPEAT 301 338
 REPEAT 341 378
 REPEAT 381 418
 REPEAT 424 461
 REPEAT 464 503
 REPEAT 505 541
 REPEAT 553 590
 VARSPLIC 17 52
 VARIANT 543 543
 VARIANT 592 592
 STRAND 176 176
 HELIX 180 183
 TURN 184 184
 HELIX 185 187
 TURN 188 188
 HELIX 190 197
 TURN 198 199
 HELIX 202 211
 HELIX 213 221
 TURN 222 223

QY	538	TYISR	542
Db	601	TYISR	605
 RESULT 12 Q5W141_HUMAN PRELIMINARY; PRT; 605 AA. AC Q5W141; DT 10-MAY-2005, integrated into UniProtKB/TrEMBL. DT 10-MAY-2005, sequence version 1. DT 07-FEB-2006, entry version 11. DE Beta-transducin repeat containing. GN Name=BTRC; ORFNames=RP11-529I10.2-001; OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC Homo. NCBI_TaxID=9606; RN [1] RP NUCLEOTIDE SEQUENCE. RA Whitehead S.; RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. [2] RN [1] RP NUCLEOTIDE SEQUENCE. RA Bird C.; RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. [3] RN [1] RP NUCLEOTIDE SEQUENCE. RA Clark S.; RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. CC CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms CC Distributed under the Creative Commons Attribution-NoDerivs License ----- DR EMBL; AL133387; CAH70020.1; -; Genomic_DNA. DR EMBL; AL445463; CAH70020.1; JOINED; Genomic DNA. DR EMBL; AL627424; CAH70020.1; JOINED; Genomic DNA. DR EMBL; AL445463; CA112963.1; -; Genomic DNA. DR DR EMBL; AL133387; CA112963.1; JOINED; Genomic DNA. DR EMBL; AL627424; CA112963.1; JOINED; Genomic DNA. DR EMBL; AL627424; CA110421.1; -; Genomic_DNA. DR EMBL; AL627424; CA141042.1; -; Genomic_DNA. DR EMBL; AL133387; CA141042.1; JOINED; Genomic DNA. DR EMBL; AL445463; CA141042.1; JOINED; Genomic DNA. DR Ensembl; ENSG00000166167; Homo sapiens. GO; GO:0006512; P:ubiquitin cycle; IEA. DR InterPro; IPR001810; F-box. DR InterPro; IPR001680; WD40. DR Pfam; PF00646; F-box; 1. DR Pfam; PF00400; WD40; 7. DR PRINTS; PR00320; GPROTEINBRPT. DR SMART; SM00256; FBOX; 1. DR SMART; SM00320; WD40; 7. DR PROSITE; PS50181; FBOX; 1. DR PROSITE; PS00678; WD_REPEATS_1; 6. DR PROSITE; PS50082; WD_REPEATS_2; 7. DR PROSITE; PS50294; WD_REPEATS_REGION; 1. KW Repeat; Ub1 conjugation pathway; WD repeat. SQ SEQUENCE 605 AA; 68867 MW; 4C67F3B7E400FD37 CRC64;			
Query Match 84.9%; Score 2445.5; DB 2; Length 605; Best Local Similarity 75.7%; Pred No. 1 4e-172; Matches 456; Conservative 49; Mismatches 35; Indels 63; Gaps 34;			
Qy	1	MEP-DVSIEDKTIELMCSPRSLWLGCANIVESCALSCL-----	39
		: : : : : : : : : : : : : : : : : : : :	
Db	1	MDPAEALVQEALKFKMCSMPRSLWLGCSSLADSMPSLRCLYNPQTGALTAFQNSSREDC	60
Qy	40	-----QSMPSVRCL---QISNGTSSVIV	59
		: :	
Db	61	NNGEPFRKI1PEKNRSURQTVNSCARCLCNQETVCLASTAMTKVCNCAKTKLANGTSMW	120
Qy	60	SRRKPSRGNTQKBDLCIKYFDQWSESDQVEFVEHLIRSMCHYOQHGINSYLKPMQLORDF	119

Db 121 PKQRKLSAYEKEKELCVYFEQSESDQVEFVHLLISOMCHYQGHINSYKPMQLQDFP 180
Qy 120 ITALPEOGLDHAENILSYLDARSILCAELVCKEQRVISSEGMLWKKLIERWRTDPLWK 179
Db 181 ITALPARGLDHAENILSYLDARSLCAELVCKEQRVYTSQDMLWKKLIERWRTDLSLR 240
Qy 180 GLSERRGWDQYLFKNRPTDG--PPNSFVRSYLPKPIQDIETESNWRGCRNLQRIQCRS 237
Db 241 GLAERGGWQYLFKNRPPGPNAPNSFVRYALPKPIQDIETESNWRGCRSLQRIHCRS 300
Qy 238 ENSKGVCYQYDDDEKIIISGLRDNSTIKWDKTSLECLKVLGTGHTGVSCLQYDERVITGS 297
Db 301 ETSKGVCYQYDDQKIVSGSLRDNSTIKWDKNTLECKRILTGTGHTGVSCLQYDERVITGS 360
Qy 298 SDSTVRVWVNTGEVNTLIHNEAVLHRSNGLMVTCSKDRSIAVWDMASATDITLRR 357
Db 361 SDSTVRVWVNTGEMNTLIHCEAVLHRSNGLMVTCSKDRSIAVWDMASPTDITLRR 420
Qy 358 VLVGHRAAVNVVDFDKYIVSASGDRITIKVWSTSTCFVRLTNGHKGRIACLOYRDLVV 417
Db 421 VLVGHRAAVNVVDFDKYIVSASGDRITIKVWSTSTCFVRLTNGHKGRIACLOYRDLVV 480
Qy 418 SGSSDNTIRLWDIEGACLRVLGHEELVRCIRFNDKRVISGAYDGKIKVWDLQALDPR 477
Db 481 SGSSDNTIRLWDIEGACLRVLGHEELVRCIRFNDKRVISGAYDGKIKVWDLVAALDPR 540
Qy 478 APASTLCURTIVHSGRVRFRLODFBQIISSHDDTILWFLNVPSPAQNETRSPSRTY 537
Db 541 APAGTLCURTIVHSGRVRFRLODFBQIIVSSSHDDTILWFLNDPAAQAQPPRSPSRTY 600
Qy 538 TYISR 542
Db 601 TYISR 605

RESULT 13
ID Q3UL2A_MOUSE PRELIMINARY; PRT; 605 AA.
AC Q3UL2A;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Blastocyst blastocyst cDNA, RIKEN full-length enriched library,
DE clone:11C02312 product:beta-transducin repeat containing protein,
DE full insert sequence.
GN Name=Btrc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
(1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Methods Enzymol. 303:19-44(1999).
(2)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels B.P., de Bono B., Della Gatta G.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,

Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
Hill D., Huminek L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
Kisano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
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Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
Mortagui-Tabar S., Mulder N., Nakano N., Nakautchi H., Ng P.,
Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
Roat B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
Schonbach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Sheng Y.,
Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
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Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome."
RL Science 309:1559-1563(2005).
(3)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome."
RL Science 309:1564-1566(2005).
(4)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanaai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kogawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
(5)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hata A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtauki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuiura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichannel capillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuiura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichannel capillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanegawa S.,
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: AK145624; BAB26547.1; -; mRNA.
 DR MGI: MGI:1339871; Btxc.
 DR GO: GO:0005783; C: endoplasmic reticulum; RCA.
 DR GO: GO:0004840; F: ubiquitin conjugating enzyme activity; RCA.
 DR GO: GO:0006464; P: protein modification; RCA.
 DR GO: GO:0007165; P: signal transduction; RCA.
 DR GO: GO:0006511; P: ubiquitin-dependent protein catabolism; RCA.
 DR InterPro: IPR001810; F-box.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00646; F-box; 1.
 DR Pfam: PF00400; WD40; 7.
 DR PRINTS: PR00320; GPROTEINRPT.
 DR PRODOM: PD000018; WD40; 4.
 DR SMART: SM00256; FBOX; 1.
 DR SMART: SM00320; WD40; 7.

DR PROSITE; PS00181; FBOX; 1.
 DR PROSITE; PS00678; WD REPEATS 1; 6.
 DR PROSITE; PS0082; WD REPEATS 2; 7.
 DR PROSITE; PS0094; WD REPEATS REGION; 1.
 KW Repeat; Ubl conjugation pathway; WD repeat.
 SQ SEQUENCE 605 AA, 68942 MW, 557B3942F52DC472 CRC64;

 Query Match 84.7%; Score 2437.5; DB 2; Length 605;
 Best Local Similarity 75.4%; Pred. No. 5.5e-172;
 Matches 456; Conservative 51; Mismatches 35; Indels 63; Gaps 4;

 QY 1 MEP-DSVIEDKTIELMCSVPRLSLGLGNCANLVSFMSCLSL-----QSMPSVRL---QISNGTSSVIV 39
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 QY 40 -----QSMPSVRL---QISNGTSSVIV 59
 DB 61 NNGEPPRKIIPEKNSLRQTYNSCARLCINQETVCLTSTAMKTENCVAKAKLANGTSSMIV 120
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 DB 121 PKQKLSASYEKELCVKYPFQWSESQDVEFVHLSIRMCYHGHINSYKPMLODF 180
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 DB 241 GLAERGWQYLFKNRPTD--GPPNSFYRSLYPKIIQDIETIESNWRCCGRHNIQOICRS 300
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 DB 361 SOSTVVRVDVNTGVLNTLIHNEAVLHLRFNSGLMTSCDKRSIAVWDMASATDITLRR 420
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 DB 481 SGSSDNTIRLWDIECCACLRVLEEGHEELVRCIRFDNKRIVSGAYDCKIKVWDLQALDPR 540
 QY 478 APASTLCRLTVHSGRVERLQDFEQIISSSHDDTLILWDFLNVPPSAQNETRSPSRTY 537
 DB 541 APAGTLCRLTVHSGRVERLQDFEQIISSSHDDTLILWDFLNVPPSAQNETRSPSRTY 600
 QY 538 TYISR 542
 DB 601 TYISR 605

 RESULT 14
 Q571K6 MOUSE
 ID Q571K6 MOUSE PRELIMINARY; PRT; 639 AA.
 AC Q571K6;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DE MKIAA4123 protein (Fragment).
 GN Name=Btrc; Synonyms=mkIAA4123;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;

RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
 RA Saga Y., Nagase T., Ohata O., Koga H.;
 RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene.
 RT The Complete Nucleotide Sequences of Mouse KIAA-homologous cDNAs
 RT Identified by Screening of Terminal sequences of cDNA Clones Randomly
 RT Sampled from Size-Fractionated Libraries.";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; AK220183; BAD90368.1; -; mRNA.
 DR Ensembl; ENSMUSG00000025217; Mus musculus.
 DR MGI; MGI:1338871; Btrc.
 DR GO; GO:0005783; C:cytoplasmic reticulum; RCA.
 DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; RCA.
 DR GO; GO:0006464; P:protein modification; RCA.
 DR GO; GO:0007165; P:signal transduction; RCA.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; RCA.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS0181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 6.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW WD repeat.
 FT NON TER
 SQ SEQUENCE 639 AA; 72569 MW; C53DE41E9A732575 CRC64;
 Query Match 84.6%; Score 2436.5; DB 2; Length 639;
 Best Local Similarity 75.4%; Pred. No. 7e-172;
 Matches 456; Conservative 50; Mismatches 36; Indels 63; Gaps 4;
 QY 1 MEP-DSVIEDKTIEMLCVPSRLWLGCANLVESMCALSCL----- 39
 DB 35 MDAEAVLQEKALKPKMPSRLWLGCSLADSPSLRCLNPGTALTAFOVNSEREDC 94
 QY 40 -----OSMPSVRCL---QISNGTSSVIV 59
 DB 95 NNGEPPRKIIPEKNSLRQTYNSCARLCINQETVCLTSTAMKTCVAKLANGTSSMIV 154
 QY 60 SRKRPSEGNQKEKDLCTIKYFDQWSESQVFEVHLISRMCHYQHGHSYLYKPKMLQKDF 119
 DB 155 PKQRKLSASYEKEKELCVKYPFQWSESQVFEVHLISQMCHYQHGHSYLYKPKMLQKDF 214
 QY 120 ITALPEQGLDHTAENILSYLDARSICAAELVCKEQRVISEGMLWKLIERVTDPLWK 179
 DB 215 ITALPARGLDHTAENILSYLDARSLCAAELVCKEWRVITSDGMLWKLIERVTDLSLR 274
 QY 180 GLSERGGWQVLFKNRPTD--GPPNSFYRSYLPKIIQIETTESNWRGCRNLQRIQCRS 237
 DB 275 GLAERGGWQVLFKNRPTDENAPPNSFYRSLYLPKIIQIETTESNWRGCRSLQRIHCRS 334
 QY 238 ENSGKVCYQVYDEKIIISGLRDNSTKIWDKTSLECLKVLGTGHTGVLQYDVERVITGS 297
 DB 335 ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKSTLECKRILTGTGHTGVLQYDVERVITGS 394
 QY 298 SDSTVRVNDVNTGEVINTLIHNEAVLHRSNGLMVTCSKDRSTAVNDMASATDILRR 357
 DB 395 SDSTVRVNDVNTGEVINTLIHNEAVLHRSNGLMVTCSKDRSTAVNDMASPTDILRR 454
 QY 358 VLVGHRAAVNVDFDKIVSASGRTIKWSTSTCEVFRTLNHGKRGIAQLQYDRLVW 417
 DB 455 VLVGHRAAVNVDFDKIVSASGRTIKWNTSTCEVFRTLNHGKRGIAQLQYDRLVW 514
 QY 418 SGSSDNTIRLWDIEGACLRVLEGGHEELVRCIRFNDKRVISGAYDGKIKVMDLQALDPR 477
 DB 515 SGSSDNTIRLWDIEGACLRVLEGGHEELVRCIRFNDKRVISGAYDGKIKVMDLMAALDPR 574

QY 478 APASTLCRLTILVHSGRVFRLQDFEFOIISSHDDTILWDFLNVPPSAQNETRSPSRITY 537
 DB 575 APAGTLCRLTILVHSGRVFRLQDFEFOIIVSSSHDDTILWDFLNDPAAHAEPSPSRITY 634
 QY 538 TYISR 542
 DB 635 TYISR 639
 RESULT 15
 Q68DSO HUMAN
 ID Q68DSO HUMAN PRELIMINARY; PRT; 564 AA.
 AC Q68DSO;
 DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Hypothetical protein DKFZp781N011.
 GS Name=DKFZp781N011;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC TISSUE=AMYGDALA;
 RG The German cDNA Consortium;
 RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; CR749295; CAH18150.1; -; mRNA.
 DR Ensembl; ENSG00000166167; Homo sapiens.
 DR GO; GO:0006512; P:ubiquitin cycle; IEA.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS0181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 6.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Hypothetical protein; Repeat; Ub conjugation pathway; WD repeat.
 SQ SEQUENCE 564 AA; 64202 MW; 5CCF0A7C5A59B5C1 CRC64;
 Query Match 84.5%; Score 2434; DB 2; Length 564;
 Best Local Similarity 80.5%; Pred. No. 9.1e-172;
 Matches 454; Conservative 41; Mismatches 33; Indels 36; Gaps 3;
 QY 15 MCSVPSRLWLGCANLVESMCALSCL-----QSNP 43
 DB 1 MCSVPSRLWLGCSLADSPSLRCLNPGTALTAFOVNSCARLCINQETVCLASTAMK 60
 QY 44 SVRCL---QISNGTSSVIVSRKPSSEGNQKEKDLCTIKYFDQWSESQVFEVHLISRM 100
 DB 61 TENCVAKTKLANGISSMLVPQRKLSASYEKEKELCVKYPFQWSESQVFEVHLISQMC 120
 QY 101 HYQHGHSYLYKPKMLQKDFITALPEQGLDHTAENILSYLDARSICAAELVCKEQRVISE 160
 DB 121 HYQHGHSYLYKPKMLQKDFITALPARGLDHTAENILSYLDARSLCAAELVCKEWRVTD 180
 QY 161 GMLWKLIERVTDPLWKGLSERGGWQVLFKNRPTD--GPPNSFYRSYLPKIIQIETTES 218
 DB 181 GMLWKLIERVTDPLWKGLSERGGWQVLFKNRPTD--GPPNSFYRSYLPKIIQIETTES 240

Qy	219	IESNWRGRHNLQRIQCRSENSKGVYCLQYDDDEKIIISGLRDNISIKIWDKTSLECLKVLTG	278
Db	241	IESNWRGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNITIKIWDKNTLECKRILTG	300
Qy	279	HTGSVLCLOYDERVIVTVWVDNVTGEVLNTHHNEAVLHLRFSNGLMVTCSK	338
Db	301	HTGSVLCLOYDERVIVTVWVDNVTGEVLNTHHNEAVLHLRFSNGLMVTCSK	360
Qy	339	DRSIAVMDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVMSTSTCEFVRT	398
Db	361	DRSIAVMDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVMSTSTCEFVRT	420
Qy	399	LNGHKRGIACLQYDRDLVWSSDNTIRLWDIECGACLRVLEEGHEELVRCIRFDNKRIYS	458
Db	421	LNGHKRGIACLQYDRDLVWSSDNTIRLWDIECGACLRVLEEGHEELVRCIRFDNKRIYS	480
Qy	459	GAYDGKIKVWDLOALDPRAPASTLCRLTLVEHSGRVFRLOQDFEQIISSSHDDTILWD	518
Db	481	GAYDGKIKVWDLVNALDPRAPAGTLCRLTLVEHSGRVFRLOQDFEQIISSSHDDTILWD	540
Qy	519	FLNVPPSAQNETRSPSRITYISR	542
Db	541	FLNDPAAQAEPSPSRITYISR	564

Search completed: August 25, 2006, 07:22:29
Job time : 307 secs

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OM protein - protein search, using sw model

Run on: August 25, 2006, 07:22:47 ; Search time 50 Seconds
(without alignments)
948.832 Million cell updates/sec

Title: US-10-665-715-16

Perfect score: 2879

Sequence: 1 MEPDSVIEDTIELMCSVPR.....PPSAQNETRSPRTTYISR 542

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pdp.*

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4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pdp.*

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7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2879	100.0	542	2	US-09-832-161-16
2	2384.5	82.8	569	2	US-09-832-161-18
3	2384.5	82.8	569	2	US-09-385-219A-2
4	2384.5	82.8	569	2	US-09-601-168B-2
5	2286.5	79.4	517	1	US-08-190-802A-30
6	2286.5	79.4	517	2	US-08-477-346-30
7	2286.5	79.4	517	2	US-08-473-089-30
8	2286.5	79.4	517	2	US-08-487-072A-30
9	643	22.3	626	2	US-09-213-888-21
10	643	22.3	626	2	US-09-328-877D-21
11	641.5	22.3	540	2	US-09-213-888-7
12	641.5	22.3	540	2	US-09-213-888-10
13	641.5	22.3	540	2	US-09-328-877D-7
14	641.5	22.3	540	2	US-09-328-877D-10
15	641.5	22.3	545	2	US-09-213-888-6
16	641.5	22.3	545	2	US-09-328-877D-6
17	641.5	22.3	553	2	US-09-213-888-5
18	641.5	22.3	553	2	US-09-328-877D-5
19	641.5	22.3	559	2	US-09-213-888-9
20	641.5	22.3	559	2	US-09-328-877D-9
21	641.5	22.3	589	2	US-09-213-888-8
22	641.5	22.3	589	2	US-09-328-877D-8
23	641.5	22.3	592	2	US-09-213-888-4
24	641.5	22.3	592	2	US-09-328-877D-4
25	641.5	22.3	627	2	US-09-213-888-3
26	641.5	22.3	627	2	US-09-328-877D-3

ALIGNMENTS

RESULT 1

US-09-832-161-16
; Sequence 16, Application US/09832161
; Patent No. 6656713

GENERAL INFORMATION:

; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Vinon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris
; APPLICANT: Yaron, Avraham

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF

; FILE REFERENCE: 860098.427

; CURRENT APPLICATION NUMBER: US/09/832,161

; CURRENT FILING DATE: 2001-04-09

; PRIOR APPLICATION NUMBER: 09/210,060

; PRIOR FILING DATE: 1998-12-10

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 16

; LENGTH: 542

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-832-161-16

Query Match 100.0%; Score 2879; DB 2; Length 542;
Best Local Similarity 100.0%; Pred. No. 6.6e-276;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPDSVIEDTIELMCSVPRSLMGLCANLVESCALSCLOSMPSVRCLOISNGTSSVVS	60
Db	1	MEPDSVIEDTIELMCSVPRSLMGLCANLVESCALSCLOSMPSVRCLOISNGTSSVVS	60
Qy	61	RKRPSEGNQYKEDLCIKYFDQWSESQVFEVHLISRMCHYQHGHSINSLKPMQLRDFI	120
Db	61	RKRPSEGNQYKEDLCIKYFDQWSESQVFEVHLISRMCHYQHGHSINSLKPMQLRDFI	120
Qy	121	TALPEQGLDHAENILSYLDARSLCAELVCKWQVISEGMLWKLIERMVTRDPLWKG	180
Db	121	TALPEQGLDHAENILSYLDARSLCAELVCKWQVISEGMLWKLIERMVTRDPLWKG	180
Qy	181	LSERRGWDQVLFKNRPTDGPNSFYSLYKPIODIETIESNRCGHNLIQRCRENS	240
Db	181	LSERRGWDQVLFKNRPTDGPNSFYSLYKPIODIETIESNRCGHNLIQRCRENS	240
Qy	241	KGVCVCLQYDDEKIIISGLRDNISIKWDKTSLECLKVLGTGHTSVLCLOYDERVITGSSDS	300

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Db 241 KGYCLQYDDEKIIISGLRDSIKIMDKTSLECLVLTGHTGSLVCLQYDERVIVTGSSDS 300
QY 301 TVRVMDVNTGEVLNTHLHNEAVLHLRFNSGLMVTCSKDRSIAVMDMASATDITLRRVLV 360
Db 301 TVRVMDVNTGEVLNTHLHNEAVLHLRFNSGLMVTCSKDRSIAVMDMASATDITLRRVLV 360
QY 361 GHRAAVNVVDFDDKYIVTSASGRTIKVMTSTCEVFTLNHGRGIACIQLYRDLRVVSGS 420
Db 361 GHRAAVNVVDFDDKYIVTSASGRTIKVMTSTCEVFTLNHGRGIACIQLYRDLRVVSGS 420
QY 421 SDNTIRLWDECGACILVLEGEHELVRCIFONKRIVSGAYDGKIKVMDLQALDPRAPA 480
Db 421 SDNTIRLWDECGACILVLEGEHELVRCIFONKRIVSGAYDGKIKVMDLQALDPRAPA 480
QY 481 STLCLRTLVEHSGRVFRLQDFEQIISSHDDTILIWDFLNVPPSAQNETRSPSRITYI 540
Db 481 STLCLRTLVEHSGRVFRLQDFEQIISSHDDTILIWDFLNVPPSAQNETRSPSRITYI 540
QY 541 SR 542
Db 541 SR 542
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RESULT 2

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US-09-832-161-18
; Sequence 18, Application US/09832161
; Patent No. 6656713
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yinon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; FILE OF INVENTION: NF-KB
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/09/832,161
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/210,060
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-161-18
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Query Match 82.8%; Score 2384.5; DB 2; Length 569;
Best Local Similarity 79.0%; Pred. No. 6.4e-227;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

QY 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLCANLV---ESMCAL 36
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QY 37 SCLQSPSVRCL---QISNGTSSVIVSRKRPSEGNVQKEKDLCKIKYFDOWSESDDQVEFVE 93
Db 61 S--TAMKTENCVAKTLANGTSSMIVPKQKLSASVEKEKELCVKPEQWSESDDQVEFVE 118
QY 94 HLISRMCHYQHGHINSYKPMQLORDFTALPEOGLDHAENILSYLDARSCLCAELVCKE 153
Db 119 HLISQCHYQHGHINSYKPMQLORDFTALPARGLDHAENILSYLDKSLCAELVCKE 178
QY 154 WQVISEGMLWKKLIERMVTRDPLWKGSLRRGWDQYLFKNRPTDG--PPNSFYRSLYPK 211
Db 179 WYRVTSQGLMWKLIERMVTRDPLWKGSLRRGWDQYLFKNRPTDG--PPNSFYRSLYPK 238
QY 212 IIQDIETIESNWRGCRHNLQICRSSENSKGVYCLQYDDDEKIIISGLRDSIKIWKDTSLE 271
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Db 239 IIQDIETIESNWRGCRHSLQRHCHSETSKGYCLQYDDQKIVSGLRDNTIKIMDKNTLE 298
QY 272 CLKVLITGHTGSLVCLQYDERVIVTGSSDSTVRVMDVNTGEVLNTHLHNEAVLHLRFNSG 331
Db 299 CKRIILTGTGSLVCLQYDERVIVTGSSDSTVRVMDVNTGEVLNTHLHNEAVLHLRFNSG 358
QY 332 LMVTCCKDRSIAVMDMASATDITLRRVLVGHRAAVNVVDFDDKYIVTSASGDRTIKVMWSTS 391
Db 359 MMVTCCKDRSIAVMDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVTSASGDRTIKVMWSTS 418
QY 392 TCEFVRTLNHGRGIACIQLYRDLRVVSGSSDNTIRLWDECGACILVLEGEHELVRCIF 451
Db 419 TCEFVRTLNHGRGIACIQLYRDLRVVSGSSDNTIRLWDECGACILVLEGEHELVRCIF 478
QY 452 DNKRIVSGAYDGKIKVMDLQALDPRAPASTLCLRTLVEHSGRVFRLQDFEQIISSHD 511
Db 479 DNKRIVSGAYDGKIKVMDLVAALDPRAPAGTLCRLTLVEHSGRVFRLQDFEQIVSSSHD 538
QY 512 DTILIWDFLNVPPSAQNETRSPSRITYISR 542
Db 539 DTILIWDFLNDPAAQAEPSPSRITYISR 569
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RESULT 3

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US-09-385-219A-2
; Sequence 2, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiau, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385,219A
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-2
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Query Match 82.8%; Score 2384.5; DB 2; Length 569;
Best Local Similarity 79.0%; Pred. No. 6.4e-227;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

QY 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLCANLV---ESMCAL 36
Db 1 MDPAAVLQEKALKFNNSSEREDCNNGEPKRIPEKNSLRQTYNSCARLCLNQETVCLA 60
QY 37 SCLQSPSVRCL---QISNGTSSVIVSRKRPSEGNVQKEKDLCKIKYFDOWSESDDQVEFVE 93
Db 61 S--TAMKTENCVAKTLANGTSSMIVPKQKLSASVEKEKELCVKPEQWSESDDQVEFVE 118
QY 94 HLISRMCHYQHGHINSYKPMQLORDFTALPEOGLDHAENILSYLDARSCLCAELVCKE 153
Db 119 HLISQCHYQHGHINSYKPMQLORDFTALPARGLDHAENILSYLDKSLCAELVCKE 178
QY 154 WQVISEGMLWKKLIERMVTRDPLWKGSLRRGWDQYLFKNRPTDG--PPNSFYRSLYPK 211
Db 179 WYRVTSQGLMWKLIERMVTRDPLWKGSLRRGWDQYLFKNRPTDG--PPNSFYRSLYPK 238
QY 212 IIQDIETIESNWRGCRHNLQICRSSENSKGVYCLQYDDDEKIIISGLRDSIKIWKDTSLE 271
Db 239 IIQDIETIESNWRGCRHSLQRHCHSETSKGYCLQYDDQKIVSGLRDNTIKIMDKNTLE 298
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QY 272 CLKVLTGHTGSLVCLQYDERVIVTGSSTVVRVMDVNTGEVNTLIHHNEAVLHLRFSNG 331
DB 239 CKRILTGTGSLVCLQYDERVIVTGSSTVVRVMDVNTGEVNTLIHHNEAVLHLRFSNG 358
QY 332 LMVTCSDRSIAVWDMASATDITLRRVLVGHRAAVNVVDVDDKYIVSASGDRTIKVMWSTS 391
DB 359 MMVTCSDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDVDDKYIVSASGDRTIKVMWSTS 418
QY 392 TCEVRLTNGHKGRIACIQYDRDLVVGSSDNTIRLWDIECGACLRVLEGEHEELVRCIRF 451
DB 419 TCEVRLTNGHKGRIACIQYDRDLVVGSSDNTIRLWDIECGACLRVLEGEHEELVRCIRF 478
QY 452 DNKRIVSGAYDGKIKVMDLQALDPRAPASTLCRLTLVEHSGRVPRLODFQFISSSHD 511
DB 479 DNKRIVSGAYDGKIKVMDLVAALDPRAPAGTLCRLTLVEHSGRVPRLODFQFISSSHD 538
QY 512 DTILWDFLNPPSAQNTRSPSRTTYISR 542
DB 539 DTILWDFLNPPSAQAEPSPSRTTYISR 569

RESULT 4
US-09-601-1688-2
; Sequence 2, Application US/096011688
; Patent No. 6730486
; GENERAL INFORMATION:
; APPLICANT: BENAROUS, Richard
; APPLICANT: MARGOTTIN, Florence
; APPLICANT: DURAND, Hervé
; APPLICANT: ARENZANA SEISDEDOS, Fernando
; APPLICANT: KROLL, Mathias
; APPLICANT: CONDORCET, Jean-Paul
; TITLE OF INVENTION: Human beta-TrCP protein
; FILE REFERENCE: 935.38812X00
; CURRENT APPLICATION NUMBER: US/09/601,168B
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: PCT/FR99/00196
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: FR98 01100
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR98 15545
; PRIOR FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1 and manually
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence : cDNA
; OTHER INFORMATION: coding for human beta-TrCP protein

US-09-601-1688-2
Query Match 82.8%; Score 2384.5; DB 2; Length 569;
Best Local Similarity 79.0%; Pred. No. 6.4e-227;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

QY 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
DB 1 MDPAAVLQKALKFPMNSEREDCNGGPPPKIIPKNSLRQTYNSCARLCLNQETVCLA 60
QY 37 SCLQSPMPSVRL---QISNGTSSVIVSRKSEGNVQKEKDLCTKYFDOWSESQVEVE 93
DB 61 S--TAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYPQWSESQVEVE 118
QY 94 HLISRMCHYQGHINSYLNKPLQDFITALPEQGLDHAENILSYLDARSICAELVCKE 153
DB 119 HLISQCHYQGHINSYLNKPLQDFITALPARGLDHAENILSYLDAKSICAELVCKE 178
QY 154 WORVISGMLWKGLIERMVRTDPLWKLGSRRGMDQYLFKNRPTDG--PPNSFYRSLYPK 211
DB 179 WYRVTSDGMLWKGLIERMVRTDSLWRGLAERRGWQYLFKNKPPDGNAPPNSFYRSLYPK 238

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QY 212 IIQDIETIESNWRGCRHNLQRIQCRSENSKGVYCLQYDDDEKIIISGLRDNISIKIWDKTSLE 271
DB 239 IIQDIETIESNWRGCRHNLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNITIKIWDKNTLE 298
QY 272 CLKVLTGHTGSLVCLQYDERVIVTGSSTVVRVMDVNTGEVNTLIHHNEAVLHLRFSNG 331
DB 299 CKRILTGTGSLVCLQYDERVIVTGSSTVVRVMDVNTGEVNTLIHHCEAVLHLRFSNG 358
QY 332 LMVTCSDRSIAVWDMASATDITLRRVLVGHRAAVNVVDVDDKYIVSASGDRTIKVMWSTS 391
DB 359 MMVTCSDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDVDDKYIVSASGDRTIKVMWSTS 418
QY 392 TCEVRLTNGHKGRIACIQYDRDLVVGSSDNTIRLWDIECGACLRVLEGEHEELVRCIRF 451
DB 419 TCEVRLTNGHKGRIACIQYDRDLVVGSSDNTIRLWDIECGACLRVLEGEHEELVRCIRF 478
QY 452 DNKRIVSGAYDGKIKVMDLQALDPRAPASTLCRLTLVEHSGRVPRLODFQFISSSHD 511
DB 479 DNKRIVSGAYDGKIKVMDLVAALDPRAPAGTLCRLTLVEHSGRVPRLODFQFISSSHD 538
QY 512 DTILWDFLNPPSAQNTRSPSRTTYISR 542
DB 539 DTILWDFLNPPSAQAEPSPSRTTYISR 569

RESULT 5
US-08-190-802A-30
; Sequence 30, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WP-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 517 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
; US-08-190-802A-30

Query Match 79.4%; Score 2286.5; DB 1; Length 517;
Best Local Similarity 87.8%; Pred. No. 2.8e-217;

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Matches	423;	Conservative	33;	Mismatches	23;	Indels	3;	Gaps	2;
Qy	44	SVRCLOISNGTSSVIVSRKRPSEGNVQKEDCLCIKYFDQMSQDQVEFVEHLISRMCHYQ	103	:	:	:	:	:	:
Db	34	TLRQTKLANGTSSMIVPKQKLSANYEKEKELCVKYFEQMSQDQVEFVEHLISRMCHYQ	93	:	:	:	:	:	:
Qy	104	HGHNSYLKPMQLORDFTALPEQGLDHIHAENILSYLDARSLCAELVCKEQRVISEGML	163	:	:	:	:	:	:
Db	94	HGHINTYLPKMLQRDFITALPARGLDHIHAENILSYLDAKSLCSAELVCKEWRVYTSQML	153	:	:	:	:	:	:
Qy	164	WKKLIERMVTDPLWKLSERRGCHWDVLFKNRPTDG--PNSFYSRLYPKLIQDIETIES	221	:	:	:	:	:	:
Db	154	WKKLIERMVTDLSLWRGLAERGWQYLFKNKPPDGKTPPNSFYRALYPKLIQDIETIES	213	:	:	:	:	:	:
Qy	222	NWRCGRINLQRIQCRSENSKGVCYCLQYDDDEKIIISGLRDNSIKIKWDTKTSLECLKVLTHGTG	281	:	:	:	:	:	:
Db	214	NWRCGRISLQRIHCRSETSKGVCYCLQYDDQKIVSGLRDNTIKIKWNTLECKRVLMGHTG	273	:	:	:	:	:	:
Qy	282	SVLCLOYDERVIVTSGSSDSTVRVWDVNTGEVNLTIHHNEAVLHLRFSNGLMWTCSDKRS	341	:	:	:	:	:	:
Db	274	SVLCLOYDERVVIITG-SDSTVRVWDVNTGEMNLTIHHCEAVLHLRFNNGMMVTCSDKRS	332	:	:	:	:	:	:
Qy	342	IAVWDMASATDITLRRVLVGHRAAVNVVDFDKKIVVSAGSDRTTIKWNSTSTCEFVRTLNG	401	:	:	:	:	:	:
Db	333	IAVWDMASATDITLRRVLVGHRAAVNVVDFDKKIVVSAGSDRTTIKWNSTSTCEFVRTLNG	392	:	:	:	:	:	:
Qy	402	HKRGIAQLOYRDLRVSGSSDNTIRLWDIECGACLRVLLEGHEELVRCIRFONKRVISGAY	461	:	:	:	:	:	:
Db	393	HKRGIAQLOYRDLRVSGSSDNTIRLWDIECGACLRVLLEGHEELVRCIRFONKRVISGAY	452	:	:	:	:	:	:
Qy	462	DGKIKVMDLQAALDPAPASTLCRLTLVEHSGSRVRLQDFDFQIISGSHDDTILIIWDFLN	521	:	:	:	:	:	:
Db	453	DGKIKVMDLVAALDPAPAGTLCRLTLVEHSGSRVRLQDFDFQIISGSHDDTILIIWDFLN	512	:	:	:	:	:	:
Qy	522	VP 523							
Db	513	DP 514							

RESULT 6

RES001 6
 US-08-477-346-30
 ; Sequence 30, Application US/08477346
 ; Patent No. 6262023
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Mochly-Rosen, Daria
 ; APPLICANT: Ron Dorit
 ;
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; TITLE OF INVENTION: Thereof
 ;
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morrison & Foerster
 ; STREET: 2000 Pennsylvania Avenue, NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006-1812
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,346
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/487,072
 ; FILING DATE: 07-JUN-1995
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 2550-0025.20
 ;
 ; TELECOMMUNICATION INFORMATION:
 ;

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-473-089-30

Query Match 79.4%; Score 2286.5; DB 2; Length 517;
Best Local Similarity 87.8%; Pred. No. 2.8e-217;
Matches 423; Conservative 33; Mismatches 23; Indels 3; Gaps 2;

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QY 44 SVRCLOISNGTSVIVSRKPESEGNYQKEDLCIKYFDOWSESDQVEFVEHLISRMCHQ 103
DB 34 TLKQTKLANGTSMIVPKORLSANYEKEKELCVYFEQMSQCDQVEFVEHLISRMCHQ 93

QY 104 HGHINSYLPMLQORDFITALPEQGLDHAENILSYLDARSCLAAELVCKEWRVISEGML 163
DB 94 HGHINTYLPMLQORDFITALPARGLDHAENILSYLDAKSLCSAELVCKEWRVTSQGL 153

QY 164 WKKLIERMVRTDPLWGLSERRGWQYLFKNRPTDG--PPNSFYRLSPKIIODIETIES 221
DB 154 WKKLIERMVRTDPLWGLSERRGWQYLFKNRPTDGKTPPNSFYRLSPKIIODIETIES 213

QY 222 NRCGRHNLQICRSENSKGVYQYDDEKIIISGLRDSIKIWDKTSLECLVLTGHTG 281
DB 214 NRCGRHSLQRIHCRSETSGVYQYDQDKIVSGLRDNTIKIWDKNTLECKRVLMGHTG 273

QY 282 SVLCLOYDERVITGSDSTVRVMDVNTGEVLTNLIHNEAVLHRLFSNGLMVTCSKRS 341
DB 274 SVLCLOYDERVITG--SDSTVRVMDVNTGEVLTNLIHNEAVLHRLFSNGLMVTCSKRS 332

QY 342 IAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVMWSTSTCEFVRLNG 401
DB 333 IAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVMWSTSTCEFVRLNG 392

QY 402 HKRGIAQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHBEELVRCIFDNKRIVSGAY 461
DB 393 HKRGIAQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHBEELVRCIFDNKRIVSGAY 452

QY 462 DGKIKVWDIQAALDPRAPASTLCRLTLVHSGRVFRLQDFEFOIISSSHDDTILIWDFFLN 521
DB 453 DGKIKVWDIQAALDPRAPASTLCRLTLVHSGRVFRLQDFEFOIISSSHDDTILIWDFFLN 512

QY 522 VP 523
DB 513 DP 514
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RESULT 8
US-08-487-072A-30
Sequence 30, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-487-072A-30

Query Match 79.4%; Score 2286.5; DB 2; Length 517;
Best Local Similarity 87.8%; Pred. No. 2.8e-217;
Matches 423; Conservative 33; Mismatches 23; Indels 3; Gaps 2;

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QY 44 SVRCLOISNGTSVIVSRKPESEGNYQKEDLCIKYFDOWSESDQVEFVEHLISRMCHQ 103
DB 34 TLKQTKLANGTSMIVPKORLSANYEKEKELCVYFEQMSQCDQVEFVEHLISRMCHQ 93

QY 104 HGHINSYLPMLQORDFITALPEQGLDHAENILSYLDARSCLAAELVCKEWRVISEGML 163
DB 94 HGHINTYLPMLQORDFITALPARGLDHAENILSYLDAKSLCSAELVCKEWRVTSQGL 153

QY 164 WKKLIERMVRTDPLWGLSERRGWQYLFKNRPTDG--PPNSFYRLSPKIIODIETIES 221
DB 154 WKKLIERMVRTDPLWGLSERRGWQYLFKNRPTDGKTPPNSFYRLSPKIIODIETIES 213

QY 222 NRCGRHNLQICRSENSKGVYQYDDEKIIISGLRDSIKIWDKTSLECLVLTGHTG 281
DB 214 NRCGRHSLQRIHCRSETSGVYQYDQDKIVSGLRDNTIKIWDKNTLECKRVLMGHTG 273

QY 282 SVLCLOYDERVITGSDSTVRVMDVNTGEVLTNLIHNEAVLHRLFSNGLMVTCSKRS 341
DB 274 SVLCLOYDERVITG--SDSTVRVMDVNTGEVLTNLIHNEAVLHRLFSNGLMVTCSKRS 332

QY 342 IAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVMWSTSTCEFVRLNG 401
DB 333 IAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVMWSTSTCEFVRLNG 392

QY 402 HKRGIAQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHBEELVRCIFDNKRIVSGAY 461
DB 393 HKRGIAQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHBEELVRCIFDNKRIVSGAY 452

QY 462 DGKIKVWDIQAALDPRAPASTLCRLTLVHSGRVFRLQDFEFOIISSSHDDTILIWDFFLN 521
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Db 453 DGKIKVLDVLAALDPRAPAGTLCRTLVHSGRFRLODFBQIVSSHDDTLIWDPLN 512
QY 522 VP 523
Db 513 DP 514

RESULT 9
US-09-213-888-21
; Sequence 21, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6 myc tagged
; OTHER INFORMATION: homo sapien
US-09-213-888-21

Query Match 22.3%; Score 643; DB 2; Length 626;
Best Local Similarity 30.2%; Pred. No. 1.9e-54;
Matches 163; Conservative 101; Mismatches 210; Indels 66; Gaps 15;
QY 4 DSVIEDKTI--ELMCSVPRSLWLGA---NLVESMCALS-----CLQSMPSVRC 47
Db 71 DLTMEQKLISEEDLNSMKRKLHGSEVRSFSLGKKPKCVSEYTSITGLVPCSATPTTFGD 130
QY 48 LOISNGTSSVIVSRK-----PSEGNVQKEKDLICIKYFDOWSESDQVFEVHLSRMCHY 102
Db 131 LRAANGQGO---QRRRITSVQPTGLQE-----WLKMFQSWGPEKLLALDELIDSCPT 182
QY 103 QHGHSYLVKPLQDFITALPEOGLDHAENILSYLDARSLCAAELVCKEQRVISEGM 162
Db 183 QVKKMMQVIEPQFQDFISLLPKE-----LALYVLSFLEPKDLLQAAQTCRYW-RILAEDN 237
QY 163 LWKKLIERMVRTDPLWKGLSERRGWDQYL-FKNRPTDGPNSFYRSLYPKIIQDIETIES 221
Db 238 L-----LWRECKEKEGIDEPHLHKKRKVIKP--GFHSPKMSAYIRQHRIDT 282
QY 222 NWRGHRNLQRCRSENSKGVYCLQYDDEKIIISGLRDSIKINDKTSLECLKVLTHGTG 281
Db 283 NWRGELKSPKV-LKGHDHVTICLQFCGNRIVSGSDNTLKWSAVTGKCLRTLVTGHTG 341
QY 282 SVLCQYDERVIVTGSSDSTVRVWDVNTGEVNTLIHNEAVLHLPFNSGLMVTCSKORS 341
Db 342 GWSSQMRDNIISGSTDRTLKVNNAETGECIHTLYGHTSTVRCMHLEKRVVSGSRDAT 401
QY 342 IAWDMASATDITLRVLVGHRAAVNVVDFDDKYIVSASGDRTIKWTSTCEFTVTLNG 401
Db 402 LRWVDIETGOCL---HVLMGHVAARVCQYDGRVVSAGYDFWVKWDPETETCLHTLQ 458
QY 402 HKRGACIQLYRDLRVLVSGSSDNTIRLWDIECGACLRVLEGHBEELVRCIRFDNKRIVSGAY 461
Db 459 HTNRVVSLOFDGIHVVSGLSDTSIRVWDVETGNCIHTLTGHOSLTSGMELKONILVSGNA 518
QY 462 DGKIKVLDVLAALDPRAPASTLCRLTV---EHSGRVFRLODFBQIVSSHDDTLIWD 518
Db 519 DSTVKIWDIKTG-----QCLQTLQGNKQHSVATCLOFNKFNVTSSDDGTGVLKWD 569

RESULT 10
US-09-328-877D-21
; Sequence 21, Application US/09328877D
; Patent No. 6730778
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877D
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6 myc tagged
; OTHER INFORMATION: homo sapien
US-09-328-877D-21

Query Match 22.3%; Score 643; DB 2; Length 626;
Best Local Similarity 30.2%; Pred. No. 1.9e-54;
Matches 163; Conservative 101; Mismatches 210; Indels 66; Gaps 15;
QY 4 DSVIEDKTI--ELMCSVPRSLWLGA---NLVESMCALS-----CLQSMPSVRC 47
Db 71 DLTMEQKLISEEDLNSMKRKLHGSEVRSFSLGKKPKCVSEYTSITGLVPCSATPTTFGD 130
QY 48 LOISNGTSSVIVSRK-----PSEGNVQKEKDLICIKYFDOWSESDQVFEVHLSRMCHY 102
Db 131 LRAANGQGO---QRRRITSVQPTGLQE-----WLKMFQSWGPEKLLALDELIDSCPT 182
QY 103 QHGHSYLVKPLQDFITALPEOGLDHAENILSYLDARSLCAAELVCKEQRVISEGM 162
Db 183 QVKKMMQVIEPQFQDFISLLPKE-----LALYVLSFLEPKDLLQAAQTCRYW-RILAEDN 237
QY 163 LWKKLIERMVRTDPLWKGLSERRGWDQYL-FKNRPTDGPNSFYRSLYPKIIQDIETIES 221
Db 238 L-----LWRECKEKEGIDEPHLHKKRKVIKP--GFHSPKMSAYIRQHRIDT 282
QY 222 NWRGHRNLQRCRSENSKGVYCLQYDDEKIIISGLRDSIKINDKTSLECLKVLTHGTG 281
Db 283 NWRGELKSPKV-LKGHDHVTICLQFCGNRIVSGSDNTLKWSAVTGKCLRTLVTGHTG 341
QY 282 SVLCQYDERVIVTGSSDSTVRVWDVNTGEVNTLIHNEAVLHLPFNSGLMVTCSKORS 341
Db 342 GWSSQMRDNIISGSTDRTLKVNNAETGECIHTLYGHTSTVRCMHLEKRVVSGSRDAT 401
QY 342 IAWDMASATDITLRVLVGHRAAVNVVDFDDKYIVSASGDRTIKWTSTCEFTVTLNG 401
Db 402 LRWVDIETGOCL---HVLMGHVAARVCQYDGRVVSAGYDFWVKWDPETETCLHTLQ 458
QY 402 HKRGACIQLYRDLRVLVSGSSDNTIRLWDIECGACLRVLEGHBEELVRCIRFDNKRIVSGAY 461
Db 459 HTNRVVSLOFDGIHVVSGLSDTSIRVWDVETGNCIHTLTGHOSLTSGMELKONILVSGNA 518
QY 462 DGKIKVLDVLAALDPRAPASTLCRLTV---EHSGRVFRLODFBQIVSSHDDTLIWD 518
Db 519 DSTVKIWDIKTG-----QCLQTLQGNKQHSVATCLOFNKFNVTSSDDGTGVLKWD 569

RESULT 11
US-09-213-888-7
; Sequence 7, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.

```

; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; TITLE OF INVENTION: Encode Them
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-213-888-7

Query Match      22.3%; Score 641.5; DB 2; Length 540;
Best Local Similarity 32.1%; Pred. No. 2.1e-54;
Matches 143; Conservative 89; Mismatches 177; Indels 37; Gaps 9;

QY 77 IKYFDQWSESQVEFVEHLISRMCHYQHGHSYKPMQLQRFITALPEQGLDHIENIL 136
Db 71 LKMFQSWGPEKLLALDELIDSCPTQVKHMMQVIEPQFQDFISLLPKE----LALYVL 126

QY 137 SYLDARSACAELVCKEQRVISEGMLWKKLIERMVTRDPLWKLGSERRGWDQYL-FKNR 195
Db 127 SFLEPKDLLQAQTCRYW-RILAEDNL-----LWREKCKEEDIDPLHIKRR 172

QY 196 PTDGPNSFVRSYLPKIIQDIETIESNWRGCRNLQRIQCRSENSGVYCLQYDDDEKIIIS 255
Db 173 KVIKP--GFTHSPKSAIYRQHRIDTNWRGELKSPKV-LKGHDDHVIITCLQFCGNRIVS 229

QY 256 GLRDSIKIWDKTSLECLVLTGHTGSLVCLQYDVERVITGSSDSTVRVMDVNTGEVLNT 315
Db 230 GSDDNLTWKVSAVTGKCLRTLVGHTGGVSSQMRDNIISGSDRTLKVWNAETGCIHT 289

QY 316 LIHNEAVLHLRFSNGLMWTCSDRSIAVWDMASATDITLRLVGHRAAVNVVDDEKYY 375
Db 290 LYGHTSTVRCMHLHKEKRVVSGSRDATLRVWDIETGQCL---HVLGMHVAACVQYDGR 346

QY 376 IVSASGDRTIKWSSTCEVFTLNHKGKGIACLOYRDLRVSGSSDNTIRLWDIECGAC 435
Db 347 VVSGAYDFMVKWDPETETCLHTLQHTNRVYSLQFDGIHVSGSLDTSIRVMDVETGNC 406

QY 436 LRVLGHEELVRCIRFDNKRIVSGAYDGKIKVMDLQAALDPRAPASTLCRLTLV---EHS 492
Db 407 IHTLGHQSILTSGMELKDNILVSGNADSTVKIWDIKTG-----QCLQTLQGNPKHQ 457

QY 493 GRVRLQDFEFOIISSSHDDTILIWD 518
Db 458 SAVTCLQFNKNFVITSSDDGTVKLWD 483

RESULT 12
US-09-213-888-10
; Sequence 10, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; TITLE OF INVENTION: Encode Them
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-213-888-7

Query Match      22.3%; Score 641.5; DB 2; Length 540;
Best Local Similarity 32.1%; Pred. No. 2.1e-54;
Matches 143; Conservative 89; Mismatches 177; Indels 37; Gaps 9;

QY 77 IKYFDQWSESQVEFVEHLISRMCHYQHGHSYKPMQLQRFITALPEQGLDHIENIL 136
Db 71 LKMFQSWGPEKLLALDELIDSCPTQVKHMMQVIEPQFQDFISLLPKE----LALYVL 126

QY 137 SYLDARSACAELVCKEQRVISEGMLWKKLIERMVTRDPLWKLGSERRGWDQYL-FKNR 195
Db 127 SFLEPKDLLQAQTCRYW-RILAEDNL-----LWREKCKEEDIDPLHIKRR 172

QY 196 PTDGPNSFVRSYLPKIIQDIETIESNWRGCRNLQRIQCRSENSGVYCLQYDDDEKIIIS 255
Db 173 KVIKP--GFTHSPKSAIYRQHRIDTNWRGELKSPKV-LKGHDDHVIITCLQFCGNRIVS 229

QY 256 GLRDSIKIWDKTSLECLVLTGHTGSLVCLQYDVERVITGSSDSTVRVMDVNTGEVLNT 315
Db 230 GSDDNLTWKVSAVTGKCLRTLVGHTGGVSSQMRDNIISGSDRTLKVWNAETGCIHT 289

QY 316 LIHNEAVLHLRFSNGLMWTCSDRSIAVWDMASATDITLRLVGHRAAVNVVDDEKYY 375
Db 290 LYGHTSTVRCMHLHKEKRVVSGSRDATLRVWDIETGQCL---HVLGMHVAACVQYDGR 346

QY 376 IVSASGDRTIKWSSTCEVFTLNHKGKGIACLOYRDLRVSGSSDNTIRLWDIECGAC 435
Db 347 VVSGAYDFMVKWDPETETCLHTLQHTNRVYSLQFDGIHVSGSLDTSIRVMDVETGNC 406

QY 436 LRVLGHEELVRCIRFDNKRIVSGAYDGKIKVMDLQAALDPRAPASTLCRLTLV---EHS 492
Db 407 IHTLGHQSILTSGMELKDNILVSGNADSTVKIWDIKTG-----QCLQTLQGNPKHQ 457

QY 493 GRVRLQDFEFOIISSSHDDTILIWD 518
Db 458 SAVTCLQFNKNFVITSSDDGTVKLWD 483

RESULT 13
US-09-328-877D-7
; Sequence 7, Application US/09328877D
; Patent No. 6730778
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; TITLE OF INVENTION: Encode Them
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877D
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-328-877D-7

Query Match      22.3%; Score 641.5; DB 2; Length 540;
Best Local Similarity 32.1%; Pred. No. 2.1e-54;
Matches 143; Conservative 89; Mismatches 177; Indels 37; Gaps 9;

QY 77 IKYFDQWSESQVEFVEHLISRMCHYQHGHSYKPMQLQRFITALPEQGLDHIENIL 136
Db 71 LKMFQSWGPEKLLALDELIDSCPTQVKHMMQVIEPQFQDFISLLPKE----LALYVL 126

QY 137 SYLDARSACAELVCKEQRVISEGMLWKKLIERMVTRDPLWKLGSERRGWDQYL-FKNR 195
Db 127 SFLEPKDLLQAQTCRYW-RILAEDNL-----LWREKCKEEDIDPLHIKRR 172

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196	Qy	PTDPPNGFYRSLYPKIIQDIETTESNWRGRHNLQRIQCRSNSKVYCLQYDDEKILS	255
173	Db	KVIKP--GFIHSPKWSAVIROHRIDTNWRGELKSPKV-LKGHDDHVIITCLOFCGNRIWS	229
256	Qy	GURDNSIKIWKDTSLECLKVLITGHTGSLVCLQYDERVIVTSSSDSTVRVMDVNTGEVLNT	315
230	Db	GSDNTLTKWMSAVTQGLRTLVGHTGGWSSQMRDNIISGSDTRTLKWNNAETGECIHT	289
316	Qy	LIHNEAVLHLRFSNGLMVTCSKORSJAVMDMASATDILRRVLVGHRAAVNVVDFDDKY	375
290	Db	LYGHTSTVRCMHLHEKRVVSGSRDATUKVMDIETGQCL---HVMGHVAARVCQVDDR	346
376	Qy	IYSASGDRTIKWWSSTCEFYRTLNGHKRGIACIQYRDRLVVSGSSDNTIRLWIDECGAC	435
347	Db	VVSGAYDFMWKWDPEITCLHTLQGHNRVYSLQFDGIHVVSGSLDTSLRVMDVETGNC	406
436	Qy	LRVLEGHEELVRCIRFDNKRIRVSGAYDGKIKVKWDLQAALDPRAPASTLCLRTLV---	492
407	Db	IHTLTGHQSLTSGMELKNILVSGNADSTVKIWDIKTG-----QCLQTLQGNKHKQ	457
493	Qy	GRVFRLOPDEFQIISSSHDDTILILWD	518
458	Db	SAVTCLOFNKNFVITSSDDGTVKLWD	483

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RESULT 14
US-09-328-877D-10
; Sequence 10, Application US/09328877D
; Patent No. 6730778
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; TITLE OF INVENTION: Encode Them
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877D
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877D-10

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Db      347 VVSGAYDFWVKWWDPETETCLHTLQCHTNRVYSLQFDGIHVWVSGSLDTSIRVWMDVETGNC 406
Qy      436 LRVLEGHEELVRCIRFDNKRIRVSGAYDGKIKVWDLQAAALDPAPASTLCRLTLV---EHS 492
Db      407 IHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTG-----QCLQTLQGNPKHQ 457
Qy      493 GRVFRLOQDFEQIISSSHDDTILWD 518
Db      458 SAVTCLOFNKNFVITSSDDGTGVKLWD 483

RESULT 15
US-09-213-888-6
; Sequence 6, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; TITLE OF INVENTION: Encode Them
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 6
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-6

Query Match      22.3%; Score 641.5; DB 2; Length 545;
Best Local Similarity 22.1%; Pred. No. 2,1e-54;
Matches 143; Conservative 177; Indels 37; Gaps 9;

Qy      77 IKVPDOWSQQDQVEFVHILSRMCHYQHGHINSYKPMLOKDFITALPEQGLDHAENIL 136
Db      76 LKMPQSWSGPEKLIALLDELIDSCPTQVQHMMQVIEPQFQDFDIFSLPKE----LALYVL 131
Qy      137 SYLDARSICALAEVLCKEQRVISEGMLWKKLIERNVVRTDPLWKGLSERRGWDQYL-FKQR 195
Db      132 SFLEPKDLLQAQTCRW-RILAEQNL-----LWREKCKEEGIDEPLHIKR 177
Qy      196 PTDGPPNSFYRSYKPIQDIETIESNWRGCRHNLQRIQCRSENSKGVYCLQYDDEKIIS 255
Db      178 KVIKP--GFTHSPKWSAYIRQHRIDTNWRGELKSPKV-LKGHDHIVITCLQFCGNRIVS 234
Qy      256 GLRNSIKIWDKTSLECLKVLVTGHTGVSVCLOYDERVILVTGSSDSTVVRVMDVNTGEVLNT 315
Db      235 GSSDDTLKWSAVTGKCLRLVVGHTGGVSSQMRDNIISGSTDRTLKVMNAETGECIHT 294
Qy      316 LIHNEAVLHLRFNGLMVTCSDKRSIAVMDMASATDITLRRVLVGHRAAVNVVDFDDKY 375
Db      295 LYGHTSVRCMHLKEKRVVSGSRDATLRWDIETGQCL--HVLMGHVAARVCQYDGRR 351
Qy      376 IVSASGDRRTIKWSTSTCEVFRTLNGHKGRTIACLOYRDLRVVSGSSDNTIPLWDIECGAC 435
Db      352 VVSGAYDFWVKWWDPETETCLHTLQCHTNRVYSLQFDGIHVWVSGSLDTSIRVWMDVETGNC 411
Qy      436 LRVLEGHEELVRCIRFDNKRIRVSGAYDGKIKVWDLQAAALDPAPASTLCRLTLV---EHS 492
Db      412 IHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTG-----QCLQTLQGNPKHQ 462
Qy      493 GRVFRLOQDFEQIISSSHDDTILWD 518
Db      463 SAVTCLOFNKNFVITSSDDGTGVKLWD 488

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Search completed: August 25, 2006, 07:24:10
Job time : 51 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 25, 2006, 07:34:43 ; Search time 185 Seconds
(without alignments)
1357.094 Million cell updates/sec

Title: US-10-665-715-16
Perfect score: 2879
Sequence: 1 MEPDSVIEDKTIELMCSVPR.....PPSAQNTRSPSRTYTVISR 542

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC Celler SID33/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
2: /EMC Celler SID33/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
3: /EMC Celler SID33/ptodata/2/pubpaa/US09_PUBCOMB.pap.*
4: /EMC Celler SID33/ptodata/2/pubpaa/US10_PUBCOMB.pap.*
5: /EMC Celler SID33/ptodata/2/pubpaa/US10B_PUBCOMB.pap.*
6: /EMC Celler SID33/ptodata/2/pubpaa/US11_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2879	100.0	542	3	US-09-832-161-16 Sequence 16, Appl
2	2879	100.0	542	4	US-10-665-715-16 Sequence 16, Appl
3	2384.5	82.8	569	3	US-09-832-161-18 Sequence 18, Appl
4	2384.5	82.8	569	4	US-10-042-417-2 Sequence 2, Appl
5	2384.5	82.8	569	4	US-10-038-010-8 Sequence 8, Appl
6	2384.5	82.8	569	4	US-10-665-715-18 Sequence 18, Appl
7	2384.5	82.8	569	5	US-10-652-928-2 Sequence 2, Appl
8	2384.5	82.8	569	5	US-10-632-150-2 Sequence 2, Appl
9	2384.5	82.8	569	6	US-11-073-485-2 Sequence 2, Appl
10	2384.5	82.8	569	6	US-11-073-470-2 Sequence 2, Appl
11	2384.5	82.8	569	6	US-11-073-457-2 Sequence 2, Appl
12	2384.5	82.8	569	6	US-11-099-691-12 Sequence 12, Appl
13	2384.5	82.8	569	6	US-11-073-460-2 Sequence 2, Appl
14	2375.5	82.5	569	4	US-10-687-732-18 Sequence 18, Appl
15	2077.5	72.2	510	6	US-11-097-143-6363 Sequence 6363, Ap
16	2002	69.5	408	4	US-10-687-732-15 Sequence 15, Appl
17	1829.5	63.5	407	4	US-10-687-732-14 Sequence 14, Appl
18	1638.5	56.9	701	4	US-10-369-493-5420 Sequence 5420, Ap
19	1525	53.0	424	4	US-10-687-732-13 Sequence 13, Appl
20	1143	39.7	265	3	US-09-764-848-30 Sequence 30, Appl
21	1143	39.7	265	4	US-10-116-016-30 Sequence 30, Appl
22	1143	39.7	265	4	US-10-222-020-30 Sequence 30, Appl
23	693.5	24.1	239	4	US-10-023-530-2 Sequence 2, Appl
24	654	22.7	1326	6	US-11-097-143-28503 Sequence 28503, A
25	654	22.7	1326	6	US-11-097-143-28506 Sequence 28506, A
26	654	22.7	1326	6	US-11-097-143-36945 Sequence 36945, A
27	643	22.3	626	3	US-09-213-888-21 Sequence 21, Appl

28	643	22.3	626	3	US-09-328-877A-21	Sequence 21, Appl
29	643	22.3	626	4	US-10-653-497-21	Sequence 21, Appl
30	643	22.3	626	4	US-10-653-517-21	Sequence 21, Appl
31	643	22.3	626	4	US-10-653-496A-21	Sequence 21, Appl
32	643	22.3	626	5	US-10-653-676A-21	Sequence 21, Appl
33	641.5	22.3	540	3	US-09-213-888-7	Sequence 7, Appl
34	641.5	22.3	540	3	US-09-328-877A-7	Sequence 7, Appl
35	641.5	22.3	540	3	US-09-328-877A-7	Sequence 7, Appl
36	641.5	22.3	540	3	US-09-328-877A-7	Sequence 7, Appl
37	641.5	22.3	540	4	US-10-245-618-14	Sequence 14, Appl
38	641.5	22.3	540	4	US-10-653-497-7	Sequence 7, Appl
39	641.5	22.3	540	4	US-10-653-497-10	Sequence 10, Appl
40	641.5	22.3	540	4	US-10-653-517-7	Sequence 7, Appl
41	641.5	22.3	540	4	US-10-653-517-10	Sequence 10, Appl
42	641.5	22.3	540	4	US-10-653-496A-7	Sequence 7, Appl
43	641.5	22.3	540	4	US-10-653-496A-7	Sequence 7, Appl
44	641.5	22.3	540	5	US-10-653-676A-7	Sequence 7, Appl
45	641.5	22.3	540	5	US-10-653-676A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-832-161-16
; Sequence 16, Application US/09832161
; Publication No. US20030166587A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yinon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/09/832,161
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/210,060
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-161-16

Query Match 100.0%; Score 2879; DB 3; Length 542;

Best Local Similarity 100.0%; Pred. No. 1.3e-244; Indels 0; Gaps 0;

Matches 542; Conservative 0; Mismatches 0;

Qy 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPFVRCLOISNGTSSVVS 60

Db 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLOSMPFVRCLOISNGTSSVVS 60

Qy 61 RRPSEGNQYQKEDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHSYKLPMLQDFI 120

Db 61 RRPSEGNQYQKEDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHSYKLPMLQDFI 120

Qy 121 TALPEGLDHIENILSYLDARSALCAELVCKEQRVISEGLMWKLLIEMVTRDPLWK 180

Db 121 TALPEGLDHIENILSYLDARSALCAELVCKEQRVISEGLMWKLLIEMVTRDPLWK 180

Qy 181 LSERRGMDQVLPKNRPTDGPNNFYSLPKIQTDTTIESNWRGHNLRQCRSENS 240

Db 181 LSERRGMDQVLPKNRPTDGPNNFYSLPKIQTDTTIESNWRGHNLRQCRSENS 240

Qy 241 KGVYCLQYDDEKIISGLRDNSIKIMDKTSLKVLTKHTGSLVCLQYDERVITVGTSSDS 300

Db 241 KGVYCLQYDDEKIISGLRDNSIKIMDKTSLKVLTKHTGSLVCLQYDERVITVGTSSDS 300

241	KGVCYCLQYDDDKIKISGLRDNISIKIWDKTSLECLKVLTCGTSVLCIQYDERVILVTCSSD	300
301	TVRVMDVNTGEVNLTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLV	360
301	TVRVMDVNTGEVNLTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLV	360
361	GHRAAVNVVDKDYIVSASGDRITIKWSTSTCFVRLNGHKGRIACIQYRDLRVVSGS	420
361	GHRAAVNVVDKDYIVSASGDRITIKWSTSTCFVRLNGHKGRIACIQYRDLRVVSGS	420
421	SDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGGIKVWDLQAAALDPRA	480
421	SDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGGIKVWDLQAAALDPRA	480
481	STLCURTLVEHSGRVRFLQFDEFQIISSSHDDTLIWDFLNVPPSAQNETRSPSRITYVI	540
481	STLCURTLVEHSGRVRFLQFDEFQIISSSHDDTLIWDFLNVPPSAQNETRSPSRITYVI	540
541	SR	542
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RESULT 2
US-10-665-715-16
; Sequence 16, Application US/10665715
; Publication No. US20040203098A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yinon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; TITLE OF INVENTION: NF-KB
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/10/665,715
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/210,060
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-665-715-16

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Query Match	100.0%;	Score 2879;	DB 4;	Length 542;
Best Local Similarity	100.0%;	Pred. No. 1.3e-244;		
Matches 542;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MEPDSVIEDKTIELWCSPVRSVLGNCANLVESMCALSCLOQMPVSRCLQISNGTSSSVTVS	60	
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Qy	61	RKRPSSEGNYYQEKDLCIKYFQWSESQDQVEFVEHLISRMCHYQGHINSYLPKMLQRDFI	120	
Db	61	RKRPSSEGNYYQEKDLCIKYFQWSESQDQVEFVEHLISRMCHYQGHINSYLPKMLQRDFI	120	
Qy	121	TALPEQGLDHTAENILSYLDARSLCAABLVCQEKQWQVISEGMLWKKLIERWVRTDPLWK	180	
Db	121	TALPEQGLDHTAENILSYLDARSLCAABLVCQEKQWQVISEGMLWKKLIERWVRTDPLWK	180	
Qy	181	LSERGGWQYLFKNRPDTGPPNSFYRSYLPKIIQDIETIESNWRGGRNLRQICRSENS	240	
Db	181	LSERGGWQYLFKNRPDTGPPNSFYRSYLPKIIQDIETIESNWRGGRNLRQICRSENS	240	
Qy	241	KGVCYQWYDDEKIIISGLRDNISIKTWKDTLSLECLKVLGTGTSVLCQYDERVIVITGSSDS	300	

241	QY	KGVCYQYDDKEIIISGLRDNSIKIWDKTSLECLKVLVTGHTSGVLCIQYDERVIVITGSSDS	300
301	QY	TVRVWDVNTGVLNTLIJHNEAVLHIFPSNGLMVTCSKDRSTAVWDMASATDITLRRVLV	360
301	DB	TVRVWDVNTGVLNTLIJHNEAVLHIFPSNGLMVTCSKDRSTAVWDMASATDITLRRVLV	360
361	QY	GHRAAVNVVDFDDKXIVSASGDRTIKWSTSTCFVRTLNGHKRGKIACIQYDRDLVWVSG	420
361	DB	GHRAAVNVVDFDDKXIVSASGDRTIKWSTSTCFVRTLNGHKRGKIACIQYDRDLVWVSG	420
421	QY	SDNTIRLWDIECGACLRVLGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQALDPRAPA	480
421	DB	SDNTIRLWDIECGACLRVLGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQALDPRAPA	480
481	QY	STLCRLTIVHSGRVFLQDFEFOIISSSHDDIILIWDFLNVPPSAQNETRSPSRITYYI	540
481	DB	STLCRLTIVHSGRVFLQDFEFOIISSSHDDIILIWDFLNVPPSAQNETRSPSRITYYI	540
541	QY	SR 542	
541	DB	SR 542	

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RESULT 3
US-09-832-161-18
; Sequence 18, Application US/09832161
; Publication No. US20030166587A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yinon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; FILE REFERENCE: NF-KB
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/09/832,161
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/210,060
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-161-18

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Query Match	82.8%;	Score	2384.5;	DB	3;	Length	569;
Best Local Similarity	79.0%;	Pred. No.	5.3e-201;				
Matches	451;	Conservative	48;	Mismatches	41;	Indels	31;
						Gaps	7
Qy	1	MEP--DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL	36				
Db	1	MDPAEAVLQKALFMMSSRRDCNCGEPKKIIPKXNSLPQYNSCARLCLNQETVCL	60				
Qy	37	SLGQSPMSVRCL---QISNGTSSVIVSRKRPSENGYQKEKDLCTIKYFPQWSES	93				
Db	61	S--TAMKTENCVAKTKLANGTSSMIVPKQKLSASYEKEKELCVKYPQWSES	118				
Qy	94	HLISRMCHYQHGHINSYVKPMLQDFITALPEQGLDHTAENILSYLDARSLCAAE	153				
Db	119	HLISQMHYQHGHINSYVKPMLQDFITALPARGUDHAENILSYLDKSKLCAAE	178				
Qy	154	WORVISEGMLWKLIERMVRTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFY	211				
Db	179	WYRVTSQGLWKLIERMVRTDSLWRGLAERGGQYLFKNKPPDGNAPPNSFY	238				
Qy	212	IIQDIETIESNWRGRHNLQRIQCRSENSKGVICYLDYDEKILISGLRNSIKIM	271				

Db 239 IIQDIETIESNRCGRHSLOIRHCRSETSGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE 298
 Qy 272 CLAVLHTGTSVLCLOYDERVIVTGSSDSTVRVMDVNTGVLNTLIHNEAVLHLRFSNG 331
 Db 299 CKRILHTGTSVLCLOYDERVIVTGSSDSTVRVMDVNTGVLNTLIHNEAVLHLRFSNG 358
 Qy 332 LMVTCSDRSIAVMDNASATDITLRRVLVGHRAAVNVVDFDDKYIIVSASGDRTIKWNTS 391
 Db 359 MMVTCSDRSIAVMDNASPTDITLRRVLVGHRAAVNVVDFDDKYIIVSASGDRTIKWNTS 418
 Qy 392 TCFVFTLNGHKGRIACLOVRDLVVGSSDNTIRLWDIECGACLRVLEHGBELVRCIRF 451
 Db 419 TCFVFTLNGHKGRIACLOVRDLVVGSSDNTIRLWDIECGACLRVLEHGBELVRCIRF 478
 Qy 452 DNKRIVSGAYDGKIKVWDLOAALDPRAPASTLCRLTLVEHSGRVFRLOQDFEFOIISSSH 511
 Db 479 DNKRIVSGAYDGKIKVWDLOAALDPRAPASTLCRLTLVEHSGRVFRLOQDFEFOIISSSH 538
 Qy 512 DTILIWDFLNVPPSAQNETRSPSRITYISR 542
 Db 539 DTILIWDFLNDPAQAEPSPSRITYISR 569

RESULT 4
 US-10-042-417-2
 ; Sequence 2, Application US/10042417
 ; Publication No. US20020123082A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pagano, M.
 ; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
 ; FILE REFERENCE: 5914-090-999
 ; CURRENT APPLICATION NUMBER: US/10/042,417
 ; CURRENT FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: 60/260,179
 ; PRIOR FILING DATE: 2001-01-5
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 569
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-042-417-2

Query Match 82.8%; Score 2384.5; DB 4; Length 569;
 Best Local Similarity 79.0%; Pred. No. 5.3e-201;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLCANLV---ESMCAL 36
 Db 1 MDPAEAVLQEKALKFNNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARCLNQETVCLA 60
 Qy 37 SCLQSMPSVRCL---QISNGTSSVIVSRKPSBGNQYQEKDLCIKYFDQWSESDQVEFVE 93
 Db 61 S--TAMKTENCVAKTLANGTSSMIVPKQKLSASVEKEKELCVKVFQWSESDQVEFVE 118
 Qy 94 HLISRMCHYQHGHINSYLPMLQORDFITALPEOGLDHIHAEINILSYLDARSLCAELVCKE 153
 Db 119 HLISQCHYQHGHINSYLPMLQORDFITALPARGLDHIHAEINILSYLDAKSLCAELVCKE 178
 Qy 154 WORVISEGMLWKKLIERMVTRDPLWGLSERRGWDQYLFKNRPTDG--PNSFYRSIYLPK 211
 Db 179 WYRVTSGLMWWKKLIERMVTRDPLWGLSERRGWDQYLFKNRPTDG--PNSFYRSIYLPK 238
 Qy 212 IIQDIETIESNRCGRHSLOIRHCRSETSGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE 271
 Db 239 IIQDIETIESNRCGRHSLOIRHCRSETSGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE 298
 Qy 272 CLAVLHTGTSVLCLOYDERVIVTGSSDSTVRVMDVNTGVLNTLIHNEAVLHLRFSNG 331
 Db 299 CKRILHTGTSVLCLOYDERVIVTGSSDSTVRVMDVNTGVLNTLIHNEAVLHLRFSNG 358
 Qy 332 LMVTCSDRSIAVMDNASATDITLRRVLVGHRAAVNVVDFDDKYIIVSASGDRTIKWNTS 391

Db 359 MMVTCSDRSIAVMDNASPTDITLRRVLVGHRAAVNVVDFDDKYIIVSASGDRTIKWNTS 418
 Qy 392 TCFVFTLNGHKGRIACLOVRDLVVGSSDNTIRLWDIECGACLRVLEHGBELVRCIRF 451
 Db 419 TCFVFTLNGHKGRIACLOVRDLVVGSSDNTIRLWDIECGACLRVLEHGBELVRCIRF 478
 Qy 452 DNKRIVSGAYDGKIKVWDLOAALDPRAPASTLCRLTLVEHSGRVFRLOQDFEFOIISSSH 511
 Db 479 DNKRIVSGAYDGKIKVWDLOAALDPRAPASTLCRLTLVEHSGRVFRLOQDFEFOIISSSH 538
 Qy 512 DTILIWDFLNVPPSAQNETRSPSRITYISR 542
 Db 539 DTILIWDFLNDPAQAEPSPSRITYISR 569

RESULT 5
 US-10-038-010-8
 ; Sequence 8, Application US/10038010
 ; Publication No. US20030040089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HYBRIGENICS
 ; APPLICANT: Pierre, Legrain
 ; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
 ; FILE REFERENCE: B4767A
 ; CURRENT APPLICATION NUMBER: US/10/038,010
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 60/259,377
 ; PRIOR FILING DATE: 2001-01-02
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 569
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: beta-TrCP1
 ; LOCATION: (1)..(569)
 ; OTHER INFORMATION:
 US-10-038-010-8

Query Match 82.8%; Score 2384.5; DB 4; Length 569;
 Best Local Similarity 79.0%; Pred. No. 5.3e-201;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLCANLV---ESMCAL 36
 Db 1 MDPAEAVLQEKALKFNNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARCLNQETVCLA 60
 Qy 37 SCLQSMPSVRCL---QISNGTSSVIVSRKPSBGNQYQEKDLCIKYFDQWSESDQVEFVE 93
 Db 61 S--TAMKTENCVAKTLANGTSSMIVPKQKLSASVEKEKELCVKVFQWSESDQVEFVE 118
 Qy 94 HLISRMCHYQHGHINSYLPMLQORDFITALPEOGLDHIHAEINILSYLDARSLCAELVCKE 153
 Db 119 HLISQCHYQHGHINSYLPMLQORDFITALPARGLDHIHAEINILSYLDAKSLCAELVCKE 178
 Qy 154 WORVISEGMLWKKLIERMVTRDPLWGLSERRGWDQYLFKNRPTDG--PNSFYRSIYLPK 211
 Db 179 WYRVTSGLMWWKKLIERMVTRDPLWGLSERRGWDQYLFKNRPTDG--PNSFYRSIYLPK 238
 Qy 212 IIQDIETIESNRCGRHSLOIRHCRSETSGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE 271
 Db 239 IIQDIETIESNRCGRHSLOIRHCRSETSGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE 298
 Qy 272 CLAVLHTGTSVLCLOYDERVIVTGSSDSTVRVMDVNTGVLNTLIHNEAVLHLRFSNG 331
 Db 299 CKRILHTGTSVLCLOYDERVIVTGSSDSTVRVMDVNTGVLNTLIHNEAVLHLRFSNG 358
 Qy 332 LMVTCSDRSIAVMDNASATDITLRRVLVGHRAAVNVVDFDDKYIIVSASGDRTIKWNTS 391
 Db 359 MMVTCSDRSIAVMDNASPTDITLRRVLVGHRAAVNVVDFDDKYIIVSASGDRTIKWNTS 418

Qy 392 TCEFVRTLNHGKGIACIQYRDLRVVSGSSDNTIRLWDIECGACLRVLGHEELVRCIRF 451
Db 419 TCEFVRTLNHGKGIACIQYRDLRVVSGSSDNTIRLWDIECGACLRVLGHEELVRCIRF 478
Qy 452 DNKRIVSGAYDGKIKWDLQAALDPRAPASTLCRLTTLVEHSGRVRLQDFQFISSHD 511
Db 479 DNKRIVSGAYDGKIKWDLQAALDPRAPAGTLCRLTTLVEHSGRVRLQDFQFISSHD 538
Qy 512 DTILWFLNVPVPSAQNETRSPSRTTYISR 542
Db 539 DTILWFLNDPAAQAEPSPSRTTYISR 569

RESULT 6

US-10-665-715-18
; Sequence 18, Application US/10665715
; Publication No. US20040203098A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yinon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/10/665,715
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/210,060
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 18
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-665-715-18

Query Match 82.8%; Score 2384.5; DB 4; Length 569;

Best Local Similarity 79.0%; Pred. No. 5.3e-201;

Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
Db 1 MDPAEAVLQEKALKFPMNSEREDCNNGEPKRIIPEKNSLRQTYNSCARCLINQETVCLA 60
Qy 37 SCLQSMPSVRCU---QISNGTSSVIVSRKRPSEGNVQYKEKOLCIKYFDOWSESQDVEFVE 93
Db 61 S--TAMKTENCVAKTKLANGTSSMIVPKQKLSASYEKEKELCVKYFEQWSESQDVEFVE 118
Qy 94 HLISRMCHYQGHINSYLPKMLQDFITALPQGLDHAENILSYLDARSICAELVCKE 153
Db 119 HLISQCHYQGHINSYLPKMLQDFITALPARGLDHAENILSYLDARSLCAELVCKE 178
Qy 154 WQVISEGMLWKKLIEMVRVTDPLWKGLSERRGWQYLFKNRPTDG--PPNSFYSLYPK 211
Db 179 WYRVTSQMLWKKLIEMVRVTDPLWGLAERRGWQYLFKNKPPDGNAPPNSFYALYPK 238
Qy 212 IIQDIETTESNRCRHNLRQICRSENSKGVYCLQYDDEKIIISGLRDNISIKIWDKTSLE 271
Db 239 IIQDIETTESNRCRHSRQIRHCRSETSKGVYCLQYDQKIVSGLRDNTIKIWDKNTLE 298
Qy 272 CLKVLGTGTVGLCLQYDERVITVTGSSDSTVRVWDVNTGEVNTLIHNEAVLHFRFNG 331
Db 299 CKRIILTGTGTVGLCLQYDERVITVTGSSDSTVRVWDVNTGEVNTLIHCEAVLHFRFNG 358
Qy 332 LMVTCSDRSIAVWDMASATDITLRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWMTS 391
Db 359 MMVTCSDRSIAVWDMASPTDITLRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWMTS 418

Qy 392 TCEFVRTLNHGKGIACIQYRDLRVVSGSSDNTIRLWDIECGACLRVLGHEELVRCIRF 451
Db 419 TCEFVRTLNHGKGIACIQYRDLRVVSGSSDNTIRLWDIECGACLRVLGHEELVRCIRF 478
Qy 452 DNKRIVSGAYDGKIKWDLQAALDPRAPASTLCRLTTLVEHSGRVRLQDFQFISSHD 511
Db 479 DNKRIVSGAYDGKIKWDLQAALDPRAPAGTLCRLTTLVEHSGRVRLQDFQFISSHD 538
Qy 512 DTILWFLNVPVPSAQNETRSPSRTTYISR 542
Db 539 DTILWFLNDPAAQAEPSPSRTTYISR 569

RESULT 7

US-10-652-928-2
; Sequence 2, Application US/10652928
; Publication No. US20050079558A1
; GENERAL INFORMATION:
; APPLICANT: Chiaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/652,928
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US/09/385,219A
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-652-928-2

Query Match 82.8%; Score 2384.5; DB 5; Length 569;

Best Local Similarity 79.0%; Pred. No. 5.3e-201;

Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
Db 1 MDPAEAVLQEKALKFPMNSEREDCNNGEPKRIIPEKNSLRQTYNSCARCLINQETVCLA 60
Qy 37 SCLQSMPSVRCU---QISNGTSSVIVSRKRPSEGNVQYKEKOLCIKYFDOWSESQDVEFVE 93
Db 61 S--TAMKTENCVAKTKLANGTSSMIVPKQKLSASYEKEKELCVKYFEQWSESQDVEFVE 118
Qy 94 HLISRMCHYQGHINSYLPKMLQDFITALPQGLDHAENILSYLDARSICAELVCKE 153
Db 119 HLISQCHYQGHINSYLPKMLQDFITALPARGLDHAENILSYLDARSLCAELVCKE 178
Qy 154 WQVISEGMLWKKLIEMVRVTDPLWKGLSERRGWQYLFKNRPTDG--PPNSFYSLYPK 211
Db 179 WYRVTSQMLWKKLIEMVRVTDPLWGLAERRGWQYLFKNKPPDGNAPPNSFYALYPK 238
Qy 212 IIQDIETTESNRCRHNLRQICRSENSKGVYCLQYDDEKIIISGLRDNISIKIWDKTSLE 271
Db 239 IIQDIETTESNRCRHSRQIRHCRSETSKGVYCLQYDQKIVSGLRDNTIKIWDKNTLE 298
Qy 272 CLKVLGTGTVGLCLQYDERVITVTGSSDSTVRVWDVNTGEVNTLIHNEAVLHFRFNG 331
Db 299 CKRIILTGTGTVGLCLQYDERVITVTGSSDSTVRVWDVNTGEVNTLIHCEAVLHFRFNG 358
Qy 332 LMVTCSDRSIAVWDMASATDITLRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWMTS 391
Db 359 MMVTCSDRSIAVWDMASPTDITLRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWMTS 418

392 TCEVFTLNGHKGACIQYRDRLVVGSSDNTIRLWDECGACLRVLGHEELVRCIRF 451
 419 TCEVFTLNGHKGACIQYRDRLVVGSSDNTIRLWDECGACLRVLGHEELVRCIRF 478
 452 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTICLRTLVEHSGRVFRQLQDFEQIISSHD 511
 479 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTICLRTLVEHSGRVFRQLQDFEQIISSHD 538
 512 DTILWDFLNVPPSAQNETRSPSRITYISR 542
 539 DTILWDFLNDPAQAEPSPSRITYISR 569

RESULT 8
 US-10-632-150-2
 ; Sequence 2, Application US/10632150
 ; Publication No. US2005025187A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chiaux, D.
 ; APPLICANT: Pagano, M.
 ; APPLICANT: Latres, E.
 ; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
 ; FILE REFERENCE: 5914-081
 ; CURRENT APPLICATION NUMBER: US/10/632,150
 ; CURRENT FILING DATE: 2003-07-30
 ; PRIOR APPLICATION NUMBER: US/09/385,219
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: 60/098,355
 ; PRIOR FILING DATE: 1998-08-28
 ; PRIOR APPLICATION NUMBER: 60/118,568
 ; PRIOR FILING DATE: 1999-02-03
 ; PRIOR APPLICATION NUMBER: 60/124,449
 ; PRIOR FILING DATE: 1999-03-15
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 569
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-632-150-2

Query Match 82.8%; Score 2384.5; DB 5; Length 569;
 Best Local Similarity 79.0%; Pred. No. 5.3e-201;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
 1 MDP-DSVIEDKTYELMCS-----VP-----RSLWLCANLV---ESMCAL 36
 1 MDP-DSVIEDKTYELMCS-----VP-----RSLWLCANLV---ESMCAL 36
 37 SCLQSPVSRCL--OISNGTSSVIVSRKPSSEGNVQKEDLCIKYFDOWSESQVEFVE 93
 61 S--TAMKTENCVAKTKLANGTSMIVPKORKLSASYEKEKELCVKFEQWSESQVEFVE 118
 94 HLISRMCHYQHGHSYLPMLQDFITALPEQGLDHAENILSYLDARSCLAAELVCKE 153
 119 HLISQWCHYQHGHSYLPMLQDFITALPARGLDHAENILSYLDARSCLAAELVCKE 178
 154 WQVISEGMLWKKLIEMVVRTDPLWGLSERRGWQYLFKNRPTDG--PPNSFYRSLYK 211
 179 WYRVTSQGLWKKLIEMVVRTDPLWGLSERRGWQYLFKNRPTDG--PPNSFYRSLYK 238
 212 IIODIETIESNRCGRHNLQRCSENSKGVYCYQDDDEKLIISGLRDNISIKWDKTSLE 271
 239 IIODIETIESNRCGRHNLQRCSENSKGVYCYQDDDEKLIISGLRDNISIKWDKTSLE 298
 272 CLKVLGTGHTGSLVCLQYDERVITGSSDSTVRVMDVNTGEVLTNLIHNEAVLHFRFNG 331
 299 CKRILGTGHTGSLVCLQYDERVITGSSDSTVRVMDVNTGEVLTNLIHNEAVLHFRFNG 358
 332 LMVTCSDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKIIVSASGDRTIKWNSTS 391
 359 MMVTCSDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKIIVSASGDRTIKWNSTS 418
 392 TCEVFTLNGHKGACIQYRDRLVVGSSDNTIRLWDECGACLRVLGHEELVRCIRF 451
 419 TCEVFTLNGHKGACIQYRDRLVVGSSDNTIRLWDECGACLRVLGHEELVRCIRF 478
 452 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTICLRTLVEHSGRVFRQLQDFEQIISSHD 511

392 TCEVFTLNGHKGACIQYRDRLVVGSSDNTIRLWDECGACLRVLGHEELVRCIRF 451
 419 TCEVFTLNGHKGACIQYRDRLVVGSSDNTIRLWDECGACLRVLGHEELVRCIRF 478
 452 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTICLRTLVEHSGRVFRQLQDFEQIISSHD 511
 479 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTICLRTLVEHSGRVFRQLQDFEQIISSHD 538
 512 DTILWDFLNVPPSAQNETRSPSRITYISR 542
 539 DTILWDFLNDPAQAEPSPSRITYISR 569

RESULT 9
 US-11-073-485-2
 ; Sequence 2, Application US/11073485
 ; Publication No. US20050208601A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pagano, M.
 ; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
 ; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
 ; FILE REFERENCE: 5914-090-999
 ; CURRENT APPLICATION NUMBER: US/11/073,485
 ; CURRENT FILING DATE: 2005-03-04
 ; PRIOR APPLICATION NUMBER: 10/042,417
 ; PRIOR FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: 60/260,179
 ; PRIOR FILING DATE: 2001-01-05
 ; NUMBER OF SEQ ID NOS: 92
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 569
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-073-485-2

Query Match 82.8%; Score 2384.5; DB 6; Length 569;
 Best Local Similarity 79.0%; Pred. No. 5.3e-201;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
 1 MDP-DSVIEDKTYELMCS-----VP-----RSLWLCANLV---ESMCAL 36
 1 MDP-DSVIEDKTYELMCS-----VP-----RSLWLCANLV---ESMCAL 36
 37 SCLQSPVSRCL--OISNGTSSVIVSRKPSSEGNVQKEDLCIKYFDOWSESQVEFVE 93
 61 S--TAMKTENCVAKTKLANGTSMIVPKORKLSASYEKEKELCVKFEQWSESQVEFVE 118
 94 HLISRMCHYQHGHSYLPMLQDFITALPEQGLDHAENILSYLDARSCLAAELVCKE 153
 119 HLISQWCHYQHGHSYLPMLQDFITALPARGLDHAENILSYLDARSCLAAELVCKE 178
 154 WQVISEGMLWKKLIEMVVRTDPLWGLSERRGWQYLFKNRPTDG--PPNSFYRSLYK 211
 179 WYRVTSQGLWKKLIEMVVRTDPLWGLSERRGWQYLFKNRPTDG--PPNSFYRSLYK 238
 212 IIODIETIESNRCGRHNLQRCSENSKGVYCYQDDDEKLIISGLRDNISIKWDKTSLE 271
 239 IIODIETIESNRCGRHNLQRCSENSKGVYCYQDDDEKLIISGLRDNISIKWDKTSLE 298
 272 CLKVLGTGHTGSLVCLQYDERVITGSSDSTVRVMDVNTGEVLTNLIHNEAVLHFRFNG 331
 299 CKRILGTGHTGSLVCLQYDERVITGSSDSTVRVMDVNTGEVLTNLIHNEAVLHFRFNG 358
 332 LMVTCSDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKIIVSASGDRTIKWNSTS 391
 359 MMVTCSDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKIIVSASGDRTIKWNSTS 418
 392 TCEVFTLNGHKGACIQYRDRLVVGSSDNTIRLWDECGACLRVLGHEELVRCIRF 451
 419 TCEVFTLNGHKGACIQYRDRLVVGSSDNTIRLWDECGACLRVLGHEELVRCIRF 478
 452 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTICLRTLVEHSGRVFRQLQDFEQIISSHD 511

[illegible]

Sequence 12, Application US/11099691
 Publication No. US20050260644A1
 GENERAL INFORMATION:
 APPLICANT: INCYTE PHARMACEUTICALS, INC.
 APPLICANT: BANDMAN, Olga
 APPLICANT: HILLMAN, Jennifer L.
 APPLICANT: LAL, Preeti
 APPLICANT: YUE, Henry
 APPLICANT: TANG, Y. Tom
 APPLICANT: PATTERSON, Chandra
 APPLICANT: BAUGHN, Mariah R.
 APPLICANT: YANG, Junming
 TITLE OF INVENTION: CELL SIGNALING PROTEINS
 FILE REFERENCE: PF-0521 PCT
 CURRENT APPLICATION NUMBER: US/11/099,691
 CURRENT FILING DATE: 2005-04-06
 PRIOR APPLICATION NUMBER: US/09/700,444
 PRIOR FILING DATE: 2002-08-26
 PRIOR APPLICATION NUMBER: 60/085,343
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/098,010
 PRIOR FILING DATE: 1998-08-26
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PERL Program
 SEQ ID NO 12
 TYPE: PRT
 LENGTH: 569
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc-feature
 OTHER INFORMATION: Incyte Clone 3239149
 US-11-099-691-12

Query Match 82.8%; Score 2384.5; DB 6; Length 569;
 Best Local Similarity 79.0%; Pred. No. 5.3e-201;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
 QY 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLCANLV---ESMCAL 36
 Db 1 MDPAEAVLQEKALKFNMSEREDCNNGEPKRIIPKNSLRQTYNSCARLCLNQEVCLA 60
 QY 37 SCLQSMPSVRLC---QISNGTSSTVIVSRKRPSEGNQYQEKDLCIKYFDQWSESQDVEFVE 93
 Db 61 S--TAMKTENCVAKTKLANGTSSMIVPKQKLSASVEKEKELCVKVFQWSESQDVEFVE 118
 QY 94 HLISRMCHYQHGHINSYLPKMLORDFITALPEOGLDHIHAENILSYLDARSLCAAEVLVCKE 153
 Db 119 HLISQWCHYQHGHINSYLPKMLORDFITALPARGLDHIHAENILSYLDAKSLCAAEVLVCKE 178
 QY 154 WQVVISSEGMLWKKLIERMVRTDPLWGLSERGWDQYLFKNRPTDG--PPNSFYRSLYPK 211
 Db 179 WYRVTS DGMWKKLIERMVRTDPLWGLSERGWDQYLFKNRPPDGNAPPNSFYRALYPK 238
 QY 212 IIQDIETIESNRCGRHNLQRIQCRSENSKGVYCYQYDDDEKIIISGLRDNISIKIWDKTSLE 271
 Db 239 IIQDIETIESNRCGRHSLQRIHCRSETSKGVYCYQYDDQKIVSGLRDNTIKIWDKNTLE 298
 QY 272 CLKVLGTGTSVLCLOYDERVIVTGSSDSTVRVWVNTGEVNTLIHNEAVLHLRFSNG 331
 Db 299 CKRILGTGTSVLCLOYDERVIVTGSSDSTVRVWVNTGEVNTLIHNEAVLHLRFSNG 358
 QY 332 LMVTCCKDRSIAVMDWASATDITLRVLVGHRAAVNVVDFDDKIVIVSASGDRTIKWNST 391
 Db 359 MMVTCCKDRSIAVMDWASPTDITLRVLVGHRAAVNVVDFDDKIVIVSASGDRTIKWNST 418
 QY 392 TCFEVRTLNGHKGKGIACQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 451
 Db 419 TCFEVRTLNGHKGKGIACQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 478
 QY 452 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTLCRLTLVEHSGRVFRFLQDFEQIISSSH 511
 Db 479 DNKRIVSGAYDGKIKVMDLVAALDPRAPAGTLCRLTLVEHSGRVFRFLQDFEQIIVSSSHD 538

QY 512 DTILWDFLNVPPSAQNSTRSPSRVTYYSR 542
 Db 539 DTILWDFLNDPAQAAPRSPSRVTYYSR 569
 RESULT 13
 US-11-073-460-2
 Sequence 2, Application US/11073460
 Publication No. US20050272066A1
 GENERAL INFORMATION:
 APPLICANT: Pagano, M.
 TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
 TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
 FILE REFERENCE: 5914-090-999
 CURRENT APPLICATION NUMBER: US/11/073,460
 CURRENT FILING DATE: 2005-03-04
 PRIOR APPLICATION NUMBER: 10/042,417
 PRIOR FILING DATE: 2002-01-07
 PRIOR APPLICATION NUMBER: 60/260,179
 PRIOR FILING DATE: 2001-01-05
 NUMBER OF SEQ ID NOS: 92
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 569
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-073-460-2

Query Match 82.8%; Score 2384.5; DB 6; Length 569;
 Best Local Similarity 79.0%; Pred. No. 5.3e-201;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
 QY 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLCANLV---ESMCAL 36
 Db 1 MDPAEAVLQEKALKFNMSEREDCNNGEPKRIIPKNSLRQTYNSCARLCLNQEVCLA 60
 QY 37 SCLQSMPSVRLC---QISNGTSSTVIVSRKRPSEGNQYQEKDLCIKYFDQWSESQDVEFVE 93
 Db 61 S--TAMKTENCVAKTKLANGTSSMIVPKQKLSASVEKEKELCVKVFQWSESQDVEFVE 118
 QY 94 HLISRMCHYQHGHINSYLPKMLORDFITALPEOGLDHIHAENILSYLDARSLCAAEVLVCKE 153
 Db 119 HLISQWCHYQHGHINSYLPKMLORDFITALPARGLDHIHAENILSYLDAKSLCAAEVLVCKE 178
 QY 154 WQVVISSEGMLWKKLIERMVRTDPLWGLSERGWDQYLFKNRPTDG--PPNSFYRSLYPK 211
 Db 179 WYRVTS DGMWKKLIERMVRTDPLWGLSERGWDQYLFKNRPPDGNAPPNSFYRALYPK 238
 QY 212 IIQDIETIESNRCGRHNLQRIQCRSENSKGVYCYQYDDDEKIIISGLRDNISIKIWDKTSLE 271
 Db 239 IIQDIETIESNRCGRHSLQRIHCRSETSKGVYCYQYDDQKIVSGLRDNTIKIWDKNTLE 298
 QY 272 CLKVLGTGTSVLCLOYDERVIVTGSSDSTVRVWVNTGEVNTLIHNEAVLHLRFSNG 331
 Db 299 CKRILGTGTSVLCLOYDERVIVTGSSDSTVRVWVNTGEVNTLIHNEAVLHLRFSNG 358
 QY 332 LMVTCCKDRSIAVMDWASATDITLRVLVGHRAAVNVVDFDDKIVIVSASGDRTIKWNST 391
 Db 359 MMVTCCKDRSIAVMDWASPTDITLRVLVGHRAAVNVVDFDDKIVIVSASGDRTIKWNST 418
 QY 392 TCFEVRTLNGHKGKGIACQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 451
 Db 419 TCFEVRTLNGHKGKGIACQYRDRLVVGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 478
 QY 452 DNKRIVSGAYDGKIKVMDLQAALDPRAPASTLCRLTLVEHSGRVFRFLQDFEQIISSSH 511
 Db 479 DNKRIVSGAYDGKIKVMDLVAALDPRAPAGTLCRLTLVEHSGRVFRFLQDFEQIIVSSSHD 538
 QY 512 DTILWDFLNVPPSAQNSTRSPSRVTYYSR 542
 Db 539 DTILWDFLNDPAQAAPRSPSRVTYYSR 569

RESULT 14
US-10-687-732-18
; Sequence 18, Application US/10687732
; Publication No. US20040171074A1
; GENERAL INFORMATION:
; APPLICANT: Orlicky, Stephen
; APPLICANT: Slicheri, Frank
; APPLICANT: Tyers, Mike
; APPLICANT: Willems, Andrew
; APPLICANT: Tang, Xiaojing
; TITLE OF INVENTION: Structures of Substrate Binding Pockets of SCF Complexes
; FILE REFERENCE: 14096.34USU1
; CURRENT APPLICATION NUMBER: US/10/687,732
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/419,606
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank/NP_033901
; DATABASE ENTRY DATE: 1998-08-04
; RELEVANT RESIDUES: (1)..(569)
US-10-687-732-18

Query Match 82.5%; Score 2375.5; DB 4; Length 569;
Best Local Similarity 78.6%; Pred. No. 3.3e-200;
Matches 449; Conservative 49; Mismatches 42; Indels 31; Gaps 7;

QY 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
Db 1 MDPAAVLQERKALFKPMNSREDCCNGEPKKIIEKNSLRQTYNSCARLCINQETVCLT 60
QY 37 SCLQMPVSRLC---QINGTSSVTVSRKRSEGNVQKEKLCIKYFPQWSESDOVEVE 93
Db 61 S--TAMKTENCVAKLANGTSSMIVPKRKLASYEKEKLCVKYFPQWSESDOVEVE 118
QY 94 HLISBCHVOCHINSYLPKMLQRFITALPQGLDHAENILSYLDARSICAABLVCCKE 153
Db 119 HLISQCHYQGHINSYLPKMLQRFITALPARGLDHAENILSYLDARSLCAABLVCCKE 178
QY 154 MQRVISEGMWKKLIERMVRTDPLWKGLSERRGDQYLFKNRPTD--GPPNSFYRSLYPK 211
Db 179 WYRVTSQGLWKKLIERMVRTDSLARGLAERGGWGYLFKNKPPDENAPPNSFYRSLYPK 238
QY 212 IIQDIETIESNRCGRHNLQRIQCRSENSKGVYCLQYDDKIIISGLRDNSTKIWDKTSLE 271
Db 239 IIQDIETIESNRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTKIWDKSTLE 298
QY 272 CLKVLTGHTGSLVCLQYDERVITVCGSSDSTVRVWVNTGEVNTLIHNEAVLHURFSG 331
Db 299 CKRIILTGHGSLVCLQYDERVITVCGSSDSTVRVWVNTGEVNTLIHNEAVLHURFSG 358
QY 332 LMVTCSDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDKYIVSASGDRTIKVMWSTS 391
Db 359 MMTVTCSDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDKYIVSASGDRTIKVMWSTS 418
QY 392 TCFVRTLNGHKGKGIACIQLYRDLRVVSGSDNTIRLWDIECGACLRVLEGHLELRCIRF 451
Db 419 TCFVRTLNGHKGKGIACIQLYRDLRVVSGSDNTIRLWDIECGACLRVLEGHLELRCIRF 478
QY 452 DNKRIVSGAYDCKIKVMDLOALDPRAPASTLCRLTVLHSGRVRFLQDFEQIISSSH 511
Db 479 DNKRIVSGAYDCKIKVMDLMAALDPRAPAGTLCRLTVLHSGRVRFLQDFEQIIVSSSH 538
QY 512 DTILWDFLNVPPSAQNETRSPRTVYISR 542
Db 539 DTILWDFLNDPAHAEPSPRTVYISR 569

RESULT 15
US-11-097-143-6363
; Sequence 6363, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6363
; LENGTH: 510
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-6363

Query Match 72.2%; Score 2077.5; DB 6; Length 510;
Best Local Similarity 80.8%; Pred. No. 5.2e-174;
Matches 384; Conservative 44; Mismatches 46; Indels 1; Gaps 1;

QY 61 RKRSEGNVQKEKLCIKYFPQWSESDOVEVEHLISRMCHYQHGHINSYLPKMLQRFI 120
Db 30 RKKSSPTQTERELCQYFPQWSESDQVDFVHLLSRMCHYQHGHINSYLPKMLQRFI 89
QY 121 TALPEQGLDHAENILSYLDARSICAABLVCKEQORVISEGMWKKLIERMVRTDPLWK 180
Db 90 TLLPIKGLDHAENILSYLDARSICAABLVCKEQORVISEGMWKKLIERMVRTDPLWK 149
QY 181 LSERRGWDQYLFKNRPTDGP--PNSFYRSLYPKIIQDIETIESNRCGRHNLQRIQCRSE 239
Db 150 LAERNMWMQYLFKPRPGQTQPHSFHRELFPKIMNDISIEENNMTGRHMLRRINCRSE 209
QY 240 SKGVYCLQYDDKIIISGLRDNSTKIWDKTSLECLKVLGTGHTGSLVCLQYDERVITVGS 299
Db 210 SKGVYCLQYDDKIIISGLRDNSTKIWDKTSLECLKVLGTGHTGSLVCLQYDDKIIIS 269
QY 300 STVRVWVNTGEVNTLIHNEAVLHURFSGNGLMVTCSKDRSIAVWDMASATDITLRRVL 359
Db 270 STVRVWVNTGEVNTLIHNEAVLHURFSGNGLMVTCSKDRSIAVWDMASATDITLRRVL 329
QY 360 VGHRAAVNVVDFDKYIVSASGDRTIKVMWSTSCEVFTLNGHKGKGIACIQLYRDLRV 419
Db 330 VGHRAAVNVVDFDKYIVSASGDRTIKVMWSTSCEVFTLNGHKGKGIACIQLYRDLRV 389
QY 420 SSDNTIRLWDIECGACLRVLEGHLELRCIRFDTKRIVSGAYDCKIKVMDLOALDPRAP 479
Db 390 SSDNSIRLWDIECGACLRVLEGHLELRCIRFDTKRIVSGAYDCKIKVMDLOALDPRAP 449
QY 480 ASTLCRLTVLHSGRVRFLQDFEQIISSSHDDTILWDFLNVPPSAQNETRSPS 534
Db 450 SNTLCLNTLVEHTGRVRLQDFEQIIVSSSHDDTILWDFLNVPPSAQNETRSPS 504

Search completed: August 25, 2006, 07:38:23
Job time : 187 secs

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OM protein - protein search, using sw model

Run on: August 25, 2006, 07:35:27 ; Search time 34 Seconds
(without alignments)

1090.736 Million cell updates/sec

Title: US-10-665-715-16

Perfect score: 2879

Sequence: 1 MEPDSVIEDKTIELMCSVPR.....PPSAQNETRSPRTYISR 542

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Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2879	100.0	542	US-10-968-871-6	Sequence 6, Appli
2	2384.5	82.8	569	US-10-968-871-3	Sequence 3, Appli
3	2384.5	82.8	569	US-11-106-014-2	Sequence 2, Appli
4	416.5	14.5	1281	US-10-449-902-42332	Sequence 42332, A
5	395	13.7	415	US-11-293-697-4324	Sequence 4324, Ap
6	329.5	11.4	317	US-11-056-3558-90488	Sequence 90488, A
7	329.5	11.4	317	US-11-056-3558-94244	Sequence 94244, A
8	327.5	11.4	422	US-11-106-014-4	Sequence 4, Appli
9	326	11.3	891	US-10-449-902-54504	Sequence 54504, A
10	323	11.2	267	US-11-056-3558-37531	Sequence 37531, A
11	323	11.2	267	US-11-056-3558-85524	Sequence 85524, A
12	323	11.2	333	US-11-056-3558-37530	Sequence 37530, A
13	323	11.2	333	US-11-056-3558-85523	Sequence 85523, A
14	323	11.2	654	US-10-449-902-50780	Sequence 50780, A
15	318.5	11.1	808	US-10-449-902-41350	Sequence 41350, A
16	308.5	10.7	319	US-11-056-3558-13097	Sequence 13097, A
17	308.5	10.7	346	US-11-056-3558-13096	Sequence 13096, A
18	292.5	10.2	1194	US-11-045-540-2	Sequence 2, Appli
19	292.5	10.2	1205	US-11-045-540-3	Sequence 3, Appli
20	289	10.0	324	US-10-449-902-36608	Sequence 36608, A
21	286.5	10.0	326	US-11-056-3558-26606	Sequence 26606, A
22	286.5	10.0	326	US-11-056-3558-38851	Sequence 38851, A
23	286.5	10.0	326	US-11-056-3558-86112	Sequence 86112, A
24	284.5	9.9	326	US-11-056-3558-24773	Sequence 24773, A
25	283.5	9.8	311	US-10-953-349-37148	Sequence 37148, A

ALIGNMENTS

RESULT 1

US-10-968-871-6

; Sequence 6, Application US/10968871

; Publication No. US20060177829A1

; GENERAL INFORMATION:

; APPLICANT: New York University

; APPLICANT: Pagano, Michele

; TITLE OF INVENTION: Methods to Identify Compounds Useful For Tumor Sensitization to

; TITLE OF INVENTION: DNA Damage

; FILE REFERENCE: 05986/0200145-US0

; CURRENT APPLICATION NUMBER: US/10/968,871

; CURRENT FILING DATE: 2004-10-18

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 542

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-968-871-6

Query Match 100.0%; Score 2879; DB 6; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.3e-224; Indels 0; Gaps 0;
Matches 542; Conservative 0; Mismatches 0;

QY	1	MEPDSVIEDKTIELMCSVPRSLWLCANLVESMCALSCLOSMPSVRCLOISNGTSSVIYS	60
DB	1	MEPDSVIEDKTIELMCSVPRSLWLCANLVESMCALSCLOSMPSVRCLOISNGTSSVIYS	60
QY	61	RKRPEGNYQKEKDIKCIKIFDQWSESDQVEFVEHLISRMCHYOHGHSYLPKMLQDFI	120
DB	61	RKRPEGNYQKEKDIKCIKIFDQWSESDQVEFVEHLISRMCHYOHGHSYLPKMLQDFI	120
QY	121	TALPEQGLDHAENTLSYLDARSLCAAEVLCKEORVISEGMLWKKLIERMVTDPLWKG	180
DB	121	TALPEQGLDHAENTLSYLDARSLCAAEVLCKEORVISEGMLWKKLIERMVTDPLWKG	180
QY	181	LSERGWDOYLFKNRPTDGPNNFYRSYLPKIIQDIETTESNRCGRHNLQICRSENS	240
DB	181	LSERGWDOYLFKNRPTDGPNNFYRSYLPKIIQDIETTESNRCGRHNLQICRSENS	240
QY	241	KGVCLOYDDEKIIISGLRDNSIKIWDKTSLECKVLGTGHTSVLCLOYDERVITGSSDS	300
DB	241	KGVCLOYDDEKIIISGLRDNSIKIWDKTSLECKVLGTGHTSVLCLOYDERVITGSSDS	300
QY	301	TVRVWDVNTGEVINTLIHNEAVLHFRSNGMLVMTCSKDRSTAVWDMASATDITLRRVLV	360
DB	301	TVRVWDVNTGEVINTLIHNEAVLHFRSNGMLVMTCSKDRSTAVWDMASATDITLRRVLV	360

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Qy 361 GHRAANVVDKXIVSASGRTIKWSTSTCFVRLNKGKGIACQYRDLVSGS 420
Db 361 GHRAANVVDKXIVSASGRTIKWSTSTCFVRLNKGKGIACQYRDLVSGS 420
Qy 421 SDNTRLWDIECGACLRVLEGGHEELVRCIRFDNKRIVSGAYDGGIKVWDLOAALDPAPA 480
Db 421 SDNTRLWDIECGACLRVLEGGHEELVRCIRFDNKRIVSGAYDGGIKVWDLOAALDPAPA 480
Qy 481 STLCLRTLVEHSGRVRFLQDFEQIISSSHDDTLIWDFLNVPSPAQNETRSPRTTYI 540
Db 481 STLCLRTLVEHSGRVRFLQDFEQIISSSHDDTLIWDFLNVPSPAQNETRSPRTTYI 540
Qy 541 SR 542
Db 541 SR 542

RESULT 2
US-10-968-871-3
; Sequence 3, Application US/10968871
; Publication No. US20060177829A1
; GENERAL INFORMATION:
; APPLICANT: New York University
; APPLICANT: Pagano, Michele
; TITLE OF INVENTION: Methods to Identify Compounds Useful For Tumor Sensitization to
; FILE REFERENCE: DNA Damage
; CURRENT APPLICATION NUMBER: 05986/0200145-USO
; CURRENT FILING DATE: 2004-10-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-968-871-3

Query Match 82.8%; Score 2384.5; DB 6; Length 569;
Best Local Similarity 79.0%; Pred. No. 2e-184;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
Db 1 MDPAEVLQEKALKFPMNSEREDCNNGEPKRIIPEKNSLRQTYNSCARCLNQETVCLA 60
Qy 37 SCLOSMPSVRCL---QISNGTSSVIVSRKRPSEGNQYQEKDLCIKYFDQWSESQDVEFVE 93
Db 61 S--TAMKTENCVAKTKLANGTSSMIVPKQKLSASYEKEKELCVKYFEQWSESQDVEFVE 118
Qy 94 HLISRMCHYQGHINSYLPKMLQDFITALPEQGLDHAENILSYLDARSICAABLVCCKE 153
Db 119 HLISQMHYQGHINSYLPKMLQDFITALPARGLDHAENILSYLDARSLCAABLVCCKE 178
Qy 154 WQVRISEGMKWKLIERWVRTDPLWGLSERRGWDQYLFKRPRTDG--PPNSFYRSLYPK 211
Db 179 WYRVTSQGLMVKKLIERWVRTDSLWRGLAERGWQYLFKKNPPDGNAPPNSFYRALYPK 238
Qy 212 IIQDIETIESNRCGRHNLQIQCRSENSKGVCYQDYDDEKIIISGLRDNISIKWDKTSLE 271
Db 239 IIQDIETIESNRCGRHSQRHCHSETSKGVCYQDYDQKIVSGLRDNTIKIWDKNTLE 298
Qy 272 CLKVLTGHTGSLVLCQYDERVITGSSDSTVRVWDVNTGEVINTLIHNEAVLHLRFPNG 331
Db 299 CKRILTGTGSLVLCQYDERVITGSSDSTVRVWDVNTGEMTLNLIHCEAVLHLRFPNG 358
Qy 332 LMVTCSDRSSTAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYLVSASGDRTIKVMWTS 391
Db 359 MMVTCSDRSSTAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYLVSASGDRTIKVMWTS 418
Qy 392 TCFEVRTNLNGKRGIAQYRDLVSGSSDNTIRLWDIECGACLRVLEGGHEELVRCIRF 451
Db 419 TCFEVRTNLNGKRGIAQYRDLVSGSSDNTIRLWDIECGACLRVLEGGHEELVRCIRF 478
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Qy 452 DNKRIVSGAYDGKIKVWDLOAALDPAPASTLCLRTLVEHSGRVRFLQDFEQIISSSH 511
Db 479 DNKRIVSGAYDGKIKVWDLOAALDPAPASTLCLRTLVEHSGRVRFLQDFEQIIVSSSH 538
Qy 512 DTILWDFLNVPSPAQNETRSPRTTYISR 542
Db 539 DTILWDFLNPAQAEPPEPSPRTTYISR 569

RESULT 3
US-11-106-014-2
; Sequence 2, Application US/11106014
; Publication No. US20060088846A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, Michele
; APPLICANT: Chiaux, Dah Sharim
; APPLICANT: Latres, Esther
; APPLICANT: Srivastava, Promod
; APPLICANT: Chandawarker, Rajiv
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
; FILE REFERENCE: OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; CURRENT APPLICATION NUMBER: US/11/106,014
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 10/632,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1997-03-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-014-2

Query Match 82.8%; Score 2384.5; DB 7; Length 569;
Best Local Similarity 79.0%; Pred. No. 2e-184;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWLGCANLV---ESMCAL 36
Db 1 MDPAEVLQEKALKFPMNSEREDCNNGEPKRIIPEKNSLRQTYNSCARCLNQETVCLA 60
Qy 37 SCLOSMPSVRCL---QISNGTSSVIVSRKRPSEGNQYQEKDLCIKYFDQWSESQDVEFVE 93
Db 61 S--TAMKTENCVAKTKLANGTSSMIVPKQKLSASYEKEKELCVKYFEQWSESQDVEFVE 118
Qy 94 HLISRMCHYQGHINSYLPKMLQDFITALPEQGLDHAENILSYLDARSICAABLVCCKE 153
Db 119 HLISQMHYQGHINSYLPKMLQDFITALPARGLDHAENILSYLDARSLCAABLVCCKE 178
Qy 154 WQVRISEGMKWKLIERWVRTDPLWGLSERRGWDQYLFKRPRTDG--PPNSFYRSLYPK 211
Db 179 WYRVTSQGLMVKKLIERWVRTDSLWRGLAERGWQYLFKKNPPDGNAPPNSFYRALYPK 238
Qy 212 IIQDIETIESNRCGRHNLQIQCRSENSKGVCYQDYDDEKIIISGLRDNISIKWDKTSLE 271
Db 239 IIQDIETIESNRCGRHSQRHCHSETSKGVCYQDYDQKIVSGLRDNTIKIWDKNTLE 298
Qy 272 CLKVLTGHTGSLVLCQYDERVITGSSDSTVRVWDVNTGEVINTLIHNEAVLHLRFPNG 331
Db 299 CKRILTGTGSLVLCQYDERVITGSSDSTVRVWDVNTGEMTLNLIHCEAVLHLRFPNG 358
Qy 332 LMVTCSDRSSTAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYLVSASGDRTIKVMWTS 391
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; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4324
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4324

Query Match      13.7%; Score 395; DB 7; Length 415;
Best Local Similarity 25.8%; Pred. No. 4.5e-24;
Matches 103; Conservative 79; Mismatches 140; Indels 78; Gaps 15;

QY 167 LIERVRTDPLW-----KGLSERGMDO-----YLFK-----NRPDGP 200
DB 44 LVEEIQKAEPLLTASRTQVKLLIQLRQELKQNSNHTFYLFKVLKAHILPLTNVALNKS 103
QY 201 PNSFVRSLYPKII-----QDIETIESNWRGHRNLORQCRSENSKGVVYCLOYDD-- 250
DB 104 GSCFITGSDYRTCKLWDPTASGEELNLE-----GHRNV-----VTAIAFNPPY 146
QY 251 -EKIISGLRDSIKIWDKTSLECLKVLGTGTSVLCLOYDER--VIVTGSSDSTVRVWDV 307
DB 147 GDKATGSDFKTKLMSVETGKYHTFRGHTAEIVCLSFNPQSTLAVATGSDMTAKLWDI 206
QY 308 NTGEVLNLIHNEAVLHFR--SNGLMVTSKORSIAVMDMASATDITLRVLVGHRAA 365
DB 207 QNGEVTYLRGHSABEIIISLFSNTSGDRIITGTFDHTVVVWDADTGRKV---NILGHCAE 263
QY 366 VNVVDF--DDKVIYASGDRTIKVWSTSTCFVRTLNGHKRGI--ACLOYRDLRVVSGSS 421
DB 264 ISSASFNWDCSLILITGSMDKTKLWDATNGKCVATLTHGDDDEILDSCFDYTGKLIATASA 323
QY 422 DNTIRLWDIECGACLRVLGHEELVRCIRFD--NKRIYSGAYDGIKIVMDLQAALDPRAP 479
DB 324 DGTARIFSAATKCIKLEGEHEGEEKISFNPOGHNHLLTGSSDKTARIWDAQTG----- 377
QY 480 ASTLCRLTVHSGRVFRLQDFEQ--IISSHDDTILIW 517
DB 378 --OCLQVLEGHTDEIFSCAFNYKGNIVITGSKONTCRIW 414

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RESULT 4

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US-10-449-902-42332
; Sequence 42332, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-393870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 42332
; LENGTH: 1281
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-42332

Query Match      14.5%; Score 416.5; DB 6; Length 1281;
Best Local Similarity 35.8%; Pred. No. 3.8e-25;
Matches 105; Conservative 49; Mismatches 104; Indels 35; Gaps 9;

QY 249 DEKIISGLRDSIKIWDKTSLECLKVLGTGTSV--LCLQYDERVIVTGSSDSTVRVWD 306
DB 746 DGQRVVSGSYDQTLRWDAATGECVRELQHTSLVFAVALSADGQRIYSGSSDLTARVWD 805
QY 307 VNTGEVLNLIHNEAVLHFRSNG--LMVTSKORSIAVMDMASATDITLRVLVGHRA 364
DB 806 TATGETLRELKGTGMVRSVAFSTDGQRIYVGTGDDQSVRVWDASTGECV---RELKGYTA 862
QY 365 AVNVVDF--DDKVIYASGDRTIKVWSTSTCFVRTLNGHKRGIACLOVR--DRLVWSSG 420
DB 863 ALISVAFSPDQRIYSGGDDQTVRVWNAATGECQELKGTQVDSIAFSPDQHIYVSGS 922
QY 421 SNTIRLWDIEC-----GACLRVLGHEELVRCIRF--DNKRIYSGAYDGIKIV 467
DB 923 IDQTLRVMDVSSLSPPSSSSSGGAGLRERQGTGKDVNSVAFPPDGRKILASGSDQSVRV 982
QY 468 WDLQALDPRAPASTLCRLTVHSGRVFRLQF--DEFQIISSHDDTILIW 518
DB 983 WD-----AVSGELLHELQHGSGWRCVFPDQRIYSGSDDTQVRLWD 1026

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RESULT 5

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US-11-293-697-4324
; Sequence 4324, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA

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RESULT 6

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US-11-056-355B-90488
; Sequence 90488, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 90488
; LENGTH: 317
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(317)
; OTHER INFORMATION: Ceres Seq. ID no. 12724103
US-11-056-355B-90488

Query Match      11.4%; Score 329.5; DB 7; Length 317;
Best Local Similarity 31.0%; Pred. No. 6.1e-19;

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	Matches	76;	Conservative	50;	Mismatches	102;	Indels	17;	Gaps	7;
Qy	238	ENSGKVYCLQYDDEKIIISGLRDNISIKIWDKTSLECLKVLTGHTGSGVLCLOYD--ERVIVT	295							
Db	71	ENGISDVAFSSDARFIVSASDDKTLKLDVETGSLIKTLIGHTNYAFCVNFPQSNMIVS	130							
Qy	296	GSSDSTVRVDVNTGEVLTLLIHNEAVLHLRFS--NGLMVTCSKDRSIAVWDMASATDI	353							
Db	131	GSPDETVRIDVTTGCKLVKPAHSDPVTAVDFNRDGSLSIVSSYDGLCRIWD--SGTGH	188							
Qy	354	TLRRVLVGHRAAVNVDPF--DDKYIVSASGDRTIKWSTSTCEFVRTLNGHKGRIACLOQ-	410							
Db	189	CVKTLIDENPPVSVFVRFPSPNGKFIPLVGLTDLTRLNLWNISSAKELKTYTGHVNAQYCISS	248							
Qy	411	----YRDLVLVVGSSDNTIRLWDTECGACLRVLGEGHEEL---VRCIRFDNKRIVSGVADG	463							
Db	249	AFSVNKGKRVVSGSEDNCVHMWELNSKKLQKLEGHTETVWNVACHPTEN-LIASGSLDK	307							
Qy	464	KIKW 468								
Db	308	TVRIW 312								

```

RESULT 7
US-11-056-355B-94244
; Sequence 94244, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 94244
; LENGTH: 317
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(317)
; OTHER INFORMATION: Ceres Seq. ID no. 12724103
US-11-056-355B-94244

```

Query Match	11.4%	Score	329.5;	DB	7;	Length	317;
Best Local Similarity	3.0%	Pred.	No. 6.1e-19;				
Matches	76;	Conservative	50;	Mismatches	102;	Indels	17;
Gaps							7;
Qy	238	ENSGVYCLQYDDEKIIISGLRDNISIKIWDKTSLECLKVLTHGTSVLCLOYD--	--ERVIVT	295			
Db	71	ENGISDVAFFSSDARFIVSASDDKTLKLDVETGSLIKTLGHTNYAFVCFNFPQSMIVS	130				
Qy	296	GSSDSTVRYWVQNTCEVLTLIHNEAVLHREFS--NGLMYTCSKDRSIAVWDMASATDI	353				
Db	131	GSFDETVRIDWVTTGCKLUKVLPAKSDPVTAVDFNRDGSLLIVSSVYDGLCRWD--	SGTGH 188				
Qy	354	TLRRVLVGHRAAVNVVDF--DDKIYIVSASGDRTIKVMSTCEFEVRTLNGHKRGACIQ-	410				
Db	189	CVKTLIDDENPVPSPVRFSPNGKFLVGTDLNLTFLMNISSAKFLKTYTGVHVAQYCISS	248				
Qy	411	----YRDLVLYVSGSSDNTIRLWDECGACLRVLEGHEEL--VRCIRFDNKRIVSGAYDG	463				
Db	249	AFSVTNGKRIYVSGSEDNCVHMWELNSKKLLQKLEGHTETVMNVACHPTYEN-LIASGSLDK	307				
Qy	464	KIKWV	468				
Db	308	TVRIW	312				

RESULT 8
US-11-106-014--4
; Sequence 4, Application US/11106014
; Publication No. US20060088846A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, Michele
; APPLICANT: Chiaur, Dah Sharim
; APPLICANT: Latres, Esther
; APPLICANT: Srivastava, Promod
; APPLICANT: Chandawarker, Rajiv
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
; OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-106-999
; CURRENT APPLICATION NUMBER: US/11/106, 014
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 10/632,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1997-03-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-014--4

Query Match	11.4%;	Score	327.5;	DB	7;	Length	422;
Best Local Similarity	22.5%;	Pred. No.	1.3e-18;				
Matches	106;	Conservative	77;	Mismatches	137;	Indels	151;
Gaps	15;						
QY	78	KYFQWSESQOVEF-----	VEHLISRMCHYQGHINSYKLEMLORDFITALPEQ	126			
DB	4	KDFETWLDNISVTPLSLTDLKQNETLDHLISLSGAVQLRHLSNNLTLLKRDFLKLLPLE	63				
QY	127	GLDHAENILSYLDARSCLAELVCKEQRVISEGMLWKKLIERNVTDPDWKGLSERRG	186				
DB	64	----LSFYLLKWLDPQTLTLCCLYSKQWNKVIS-----	ACTEVWQTACKNLG	106			
QY	187	WDQYLFKNRPDPGPNPF-VRSLYPKIKIIDIETIESNWRGRHNLQROCRSENSKGYVC	245				
DB	107	W-----QIDDSVODAHUKVYKALKRMKQLEDH-----	136				
QY	246	LQYDDEKIIISGLRDNISKIMDKTSLECLKVLGTGTSVCLQYDERVIVTGSSTVVRW	305				
DB	137	-----EAPETSS-----	LIGHSARVYALYKDGLLCTGSDDLASKLM	173			
QY	306	DVNTGEVLNTLIHNEAVLHLRPNGLMVTCSKDRSIATVWDMASATDITLRRVLVGHRAA	365				
DB	174	DVSTGCQCYGIQTH-----TCA-----	190				
QY	366	VNVYDFDDKYIVSASGDRTIKWVSTSTCEFVRTLNHGHRKIACIQYRDL--	VVYSGSDN	423			
DB	191	--AKVFDEKLVTSQFNTVACWEMWSSGARTQHFRGHTGAVFSVDYNDLDELIVYSGSADF	248				
QY	424	TIRLWIDECGACLRVLEGHEE-----LVRC-----	IRFDNKRIVSGAYDGKIKVWDLOA	472			
DB	249	TKVWMAISAGTCLNLTLTGHTETWTVTKVWLQCKVKVKSLLHSPGDIYLLSADKYEIKWPIGR	308				
QY	473	ALDPRAPASTCLRTLVEHSGRVF-----	RLQFDEFQIISSSHDDTILIWDF	519			
DB	309	EINCK-----CLKTLVSVEDRSCLQPRLHFDGKYIVCSSALG-LQWDF	352				
RESULT	9						

US-10-449-902-54504
; Sequence 54504, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: NOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54504
; LENGTH: 891
; TYPE: prt
; ORGANISM: Oryza sativa
US-10-449-902-54504

Query Match 11.3%; Score 326; DB 6; Length 891;
Best Local Similarity 27.4%; Pred. No. 4.7e-18;
Matches 80; Conservative 61; Mismatches 119; Indels 32; Gaps 9;

Qy 249 DDEKIISGLRDSIKIWDKTSLECLKVLGTGHTGSLVCL-----QYDERVIVTGGSDSTVR 303
Db 378 DEQYLAATNLEQVRVYDVASMSCSVYLSGHTTEIVCCTICISSGKTLVVTGSKDSTVR 437
Qy 304 VMDVNTGEVLTILIHNEAVLHLRF---SNGLMVTCKDRSIAMW-----DMASATDI 353
Db 438 LMDWERRSCIGIGKGLHGAIGSVAFSKSKNFVSGSSDRTIKINSWDDTLDDVGSEVPL 497
Qy 354 TURVLVGHRAAVN--VDPFDKIIYVSGDRTIKWSTSTCEVFTTLNGHKGRIACLOQ 411
Db 498 KAKAVAAHDKDITSLNSLSPNDGLVCGSGEDRTACIWKLPNLVPSVWLKHKRGIWSVEF 557
Qy 412 R--DRLVVSGSDNTIRLWDIECGACLRVLEGHEELVRCIRP--DNKRIVSGAYDGIKV 467
Db 558 SPVEQCVTSSGDRTVKIMAWADGSCCLKTFEGHTSSVLRASFLSHGTQFVSGGSDGLVKL 617
Qy 468 WDLQAALDPAPASTLCLTLTVHSGRVPRLQF-DEFQIISSSHDDTTL-IW 517
Db 618 WTIK-----TNECIATFDKDKQWALAVGKKTEMLATGGTDAVLNLW 660

RESULT 10
US-11-056-355B-37531
; Sequence 37531, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 37531
; LENGTH: 267
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(267)
; OTHER INFORMATION: Ceres Seq. ID no. 12335591
US-11-056-355B-37531

Query Match 11.2%; Score 323; DB 7; Length 267;
Best Local Similarity 30.6%; Pred. No. 1.6e-18;
Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;

Qy 223 WRCGRHNLQRIQCRSENGKGVYCLQY--DDEKIISGLRDSIKIWD-KTSLECLKVLGTGH 279
Db 4 WSNATVSL--IHRYEGHSGISDLAWSSDSHYTCSASDDCTLRWDARSPEYCLKVLGRH 61
Qy 280 TGSVLCLOYD--ERVIVTGGSDSTVRVMDVNTGEVLTILIHNEAV--LHURFNGMLMT 335
Db 62 TNFVFCVNFNPPSNLIVSGSFDETIRIWEVTKGCKVRMIKAHSPMISSVHFNRDGLSIV 121
Qy 336 CSKDRSIAVDMASATDITLRVLVGHRAAVNVDF--DDKVIYVSASGDRTIKVMSTSTC 393
Db 122 ASHDGCKIWDAKEGT--CLKTLIDDKSPAVSFAKFSPNGKFIIVATLIDSTLKLNSYATG 179
Qy 394 EFVRTLNGHKGRIACLOQ-----YRDLRVVSGSDNTIRLWDIECGACLRVLEGHEEL--- 445
Db 180 KFLKVYTGHTNKVFCITSAFSVTNGKIVSGSDNCVYVLDLQARNILQRLLEGHTDAVIS 239
Qy 446 VRCIRPDNKRIVSGAY-DGKIKVWDLQA 472

US-11-056-355B-85524
; Sequence 85524, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 85524
; LENGTH: 267
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(267)
; OTHER INFORMATION: Ceres Seq. ID no. 12680898
US-11-056-355B-85524

Query Match 11.2%; Score 323; DB 7; Length 267;
Best Local Similarity 30.6%; Pred. No. 1.6e-18;
Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;

Qy 223 WRCGRHNLQRIQCRSENGKGVYCLQY--DDEKIISGLRDSIKIWD-KTSLECLKVLGTGH 279
Db 4 WSNATVSL--IHRYEGHSGISDLAWSSDSHYTCSASDDCTLRWDARSPEYCLKVLGRH 61
Qy 280 TGSVLCLOYD--ERVIVTGGSDSTVRVMDVNTGEVLTILIHNEAV--LHURFNGMLMT 335
Db 62 TNFVFCVNFNPPSNLIVSGSFDETIRIWEVTKGCKVRMIKAHSPMISSVHFNRDGLSIV 121
Qy 336 CSKDRSIAVDMASATDITLRVLVGHRAAVNVDF--DDKVIYVSASGDRTIKVMSTSTC 393
Db 122 ASHDGCKIWDAKEGT--CLKTLIDDKSPAVSFAKFSPNGKFIIVATLIDSTLKLNSYATG 179
Qy 394 EFVRTLNGHKGRIACLOQ-----YRDLRVVSGSDNTIRLWDIECGACLRVLEGHEEL--- 445
Db 180 KFLKVYTGHTNKVFCITSAFSVTNGKIVSGSDNCVYVLDLQARNILQRLLEGHTDAVIS 239
Qy 446 VRCIRPDNKRIVSGAY-DGKIKVWDLQA 472

```
Db 240 VSCHPVQNEISSGNHLDKTIIRWKQDA 267

RESULT 12
US-11-056-355B-37530
; Sequence 37530, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590FUS2
; CURRENT APPLICATION NUMBER: US/11/056.355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 37530
; LENGTH: 333
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(333)
; OTHER INFORMATION: Ceres Seq. ID no. 12335590
US-11-056-355B-37530

Query Match 11.2%; Score 323; DB 7; Length 333;
Best Local Similarity 30.6%; Pred. No. 2.2e-18;
Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;

Qy 223 WRCGRHNLRIQCRSENSKGYVCLQY--DDEKIISGLRDSIKIWD--KTSLECLKVLTHG 279
Db 70 WSATNYSL--IHRVEGHSSGISDLAWSSDSHYTCSASDDCTLRWDARSPEYCLKVLRGH 127
Qy 280 TGSVLCLOYD--ERVIVTSSDSTVRVWDVNTGEVLTNLHNEAV--LHLRFSNGLMVT 335
Db 128 TNFVFCVNFNPNSNLIVSGSFDETIIRWEVTKGKVRMIKAHSMPISSVHFNRDGLSV 187
Qy 336 CSKDRSIADVMDASATDITLRRVLVGHRAAVNVVDF--DDKYIVSAGDRTIKVWSTSTC 393
Db 188 ASHGGCKIWDKEGT--CLKTLIDDKSPAVSPAKFSPNGKFLVATLDSLTLSNYATG 245
Qy 394 EFVRTLNGHKGRIACLOQ-----YRDLRVSGSSDNTIRLWDIEGACLRVLEGHEEL--- 445
Db 246 KFLKVTYTGHTNKVFCITSAPSVTNGKIVSGSDNCVYLWDLQARNILQRLGHTDAVIS 305
Qy 446 VRCIRFDNKRIVSGAY-DGKIKVWDLOA 472
Db 306 VSCHPVQNEISSGNHLDKTIIRWKQDA 333

RESULT 13
US-11-056-355B-85523
; Sequence 85523, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590FUS2
; CURRENT APPLICATION NUMBER: US/11/056.355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 85523
; LENGTH: 333
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
```

```
; NAME/KEY: peptide
; LOCATION: (1)..(333)
; OTHER INFORMATION: Ceres Seq. ID no. 12680897
US-11-056-355B-85523

Query Match 11.2%; Score 323; DB 7; Length 333;
Best Local Similarity 30.6%; Pred. No. 2.2e-18;
Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;

Qy 223 WRCGRHNLRIQCRSENSKGYVCLQY--DDEKIISGLRDSIKIWD--KTSLECLKVLTHG 279
Db 70 WSATNYSL--IHRVEGHSSGISDLAWSSDSHYTCSASDDCTLRWDARSPEYCLKVLRGH 127
Qy 280 TGSVLCLOYD--ERVIVTSSDSTVRVWDVNTGEVLTNLHNEAV--LHLRFSNGLMVT 335
Db 128 TNFVFCVNFNPNSNLIVSGSFDETIIRWEVTKGKVRMIKAHSMPISSVHFNRDGLSV 187
Qy 336 CSKDRSIADVMDASATDITLRRVLVGHRAAVNVVDF--DDKYIVSAGDRTIKVWSTSTC 393
Db 188 ASHGGCKIWDKEGT--CLKTLIDDKSPAVSPAKFSPNGKFLVATLDSLTLSNYATG 245
Qy 394 EFVRTLNGHKGRIACLOQ-----YRDLRVSGSSDNTIRLWDIEGACLRVLEGHEEL--- 445
Db 246 KFLKVTYTGHTNKVFCITSAPSVTNGKIVSGSDNCVYLWDLQARNILQRLGHTDAVIS 305
Qy 446 VRCIRFDNKRIVSGAY-DGKIKVWDLOA 472
Db 306 VSCHPVQNEISSGNHLDKTIIRWKQDA 333

RESULT 14
US-10-449-902-50780
; Sequence 50780, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449.902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383670
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50780
; LENGTH: 654
; TYPE: prt
; ORGANISM: Oryza sativa
US-10-449-902-50780

Query Match 11.2%; Score 323; DB 6; Length 654;
Best Local Similarity 25.9%; Pred. No. 5.4e-18;
Matches 86; Conservative 55; Mismatches 103; Indels 88; Gaps 12;

Qy 242 GVCV--LQYDDEKIISGLRDSIKIWD-----KTS-----LE 271
Db 338 GLNCSSISHDGLSVVGGFSDSSVKVWDMKIGPPKTSPPQGENGLSGQERTSASDYKGR 397
Qy 272 CLKVLJTGHTGSLVLCLOYDE--RVIVTSSDSTVRVWDVNTGEVLTNLHNEAVLHLRFS 329
Db 398 PYTLFQHGSGPVYSAFSPFCDFLLSSSDSTIRLW-----STKLNAN----- 440
Qy 330 NGLMVTCSKDRSIADVMDASATDITLRRVLVGHRAAVNVVDFDDDKYIVSAGDRTIKVWS 389
Db 441 ----LVCYKGHPVWDVQFSP-----VGH-----YFASASHDRTAIRWS 476
Qy 390 TSTCEFVRTLNGHKKRIACLOQ--RDLRVSGSSDNTIRLWDIEGACLRVLEGHEELVR 447
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